GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: December 13, 2004, 19:35:05 ; Search time 151 Seconds
(without alignments)
171.050 Million cell updates/sec

Title: US-10-087-273-1
Perfect score: 391
Sequence: 1 TELRCQCIRTHSTPFHPKFI.....EKWVQKVVQVFVKRAEKQDP 72

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	391	100.0	72	5	ABB79966	Abb79966 CXCL8(3-7
2	388	99.2	72	5	ABB79964	Abb79964 Bovine CX
3	382	97.7	72	5	ABB79967	Abb79967 CXCL8(3-7
4	382	97.7	72	5	ABB79965	Abb79965 Bovine CX
5	366	93.6	72	5	ABB79969	Abb79969 CXCL8(3-7
6	357	91.3	72	5	ABB79968	Abb79968 CXCL8(3-7
7	312	79.8	103	3	AAB07714	Aab07714 Amino aci
8	293	74.9	72	4	AAB86153	Aab86153 Human int
9	292	74.7	72	2	AAW25706	Aaw25706 Mutant hu
10	290	74.2	69	2	AAR38081	Aar38081 Modified
11	290	74.2	72	2	AAR38080	Aar38080 Human int
12	288	73.7	72	2	AAW25704	Aaw25704 Mutant hu
13	288	73.7	72	2	AAW25705	Aaw25705 Mutant hu
14	287	73.4	71	5	ABG30773	Abg30773 1ILP comp
15	287	73.4	72	1	AAP81838	Aap81838 Sequence
16	287	73.4	72	1	AAP90913	Aap90913 Sequence
17	287	73.4	72	1	AAW26204	Aaw26204 Neutrophi
18	287	73.4	72	2	AAR03615	Aar03615 Human neu
19	287	73.4	72	2	AAR03166	Aar03166 Human neu
20	287	73.4	72	2	AAR70183	Aar70183 Soluble i
21	287	73.4	72	2	AAR88057	Aar88057 Human int
22	287	73.4	72	2	AAW25701	Aaw25701 Mutant hu
23	287	73.4	72	2	AAW12435	Aaw12435 Chimeric
24	287	73.4	72	2	AAW70289	Aaw70289 Interleuk
25	287	73.4	72	2	AAW41519	Aaw41519 Neutrophi
26	287	73.4	72	2	AAY24937	Aay24937 Neutrophi
27	287	73.4	72	5	AAE29166	Aae29166 Human int
28	287	73.4	72	6	ABG73910	Abg73910 Human Neu
29	287	73.4	72	7	ADE80881	Ade80881 IL-8 chem
30	287	73.4	72	7	ADF17069	Adf17069 Human alb
31	287	73.4	73	1	AAP90078	Aap90078 Human neu
32	287	73.4	73	2	AAR99814	Aar99814 Interleuk
33	287	73.4	73	3	AAY83202	Aay83202 Synthetic
34	287	73.4	73	6	ABU09837	Abu09837 Full leng
35	287	73.4	73	6	ABG71884	Abg71884 Human Int
36	287	73.4	76	2	AAW96737	Aaw96737 Maltose b
37	287	73.4	76	6	ABU67740	Abu67740 Factor Xa
38	287	73.4	76	7	ABO07374	Abo07374 Amino aci
39	287	73.4	77	1	AAP90017	Aap90017 Human neu
40	287	73.4	77	2	AAR13168	Aar13168 {Ala IL-8
41	287	73.4	77	3	AAY69029	Aay69029 Amino aci
42	287	73.4	77	5	AAO20027	Aao20027 Human che
43	287	73.4	77	5	AAO14160	Aao14160 Human IL-
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ALIGNMENTS

RESULT 1
ABB79966
ID ABB79966 standard; protein; 72 AA.
XX
AC ABB79966;
XX
DT 19-DEC-2002 (first entry)
XX
DE CXCL8(3-73)K11R/G31P, ELR-CXC chemokine receptor antagonist.
XX
KW ELR-CXC; chemokine; receptor; antagonist; CXCL8; cattle;
KW antiinflammatory; vasotropic; antibacterial; nephrotropic; mutant;
KW mutein.
XX
OS Bos taurus.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 9
FT /note= "wild-type Lys substituted by Arg"
FT Misc-difference 29
FT /note= "wild-type Gly substituted by Pro"
XX
PN WO200270565-A2.
XX
PD 12-SEP-2002.
XX
PF 01-MAR-2002; 2002WO-CA000271.
XX
PR 01-MAR-2001; 2001US-0273181P.
XX
PA (UYSA-) UNIV SASKATCHEWAN TECHNOLOGIES INC.
XX
PI Gordon JR, Li F;
XX
DR WPI; 2002-723251/78.
DR N-PSDB; ABQ81434.
XX
PT New ELR-CXC chemokine antagonist, useful for treating a CXC chemokine-
PT mediated pathology, e.g. ischemia-reperfusion injury or endotoxemia-
PT induced acute respiratory distress syndrome.
XX
PS Disclosure; Page 60-61; 64pp; English.
XX
CC The present sequence is the protein sequence of a mutated bovine bovine
CC CXCL8 protein comprising amino acids 3-73 of the wild-type sequence with
CC substitution of the native Gly-31 amino acid residue by Pro, and
CC substitution of the native Lys-11 residue by Arg. Claimed ELR-CXC

```
CC   chemokine antagonists of the invention comprise an amino acid
CC   substantially equivalent to a wild-type bovine CXCL8 sequence, but having
CC   a truncation of the first 2 amino acid residues of bovine CXCL8, and
CC   having the following amino acid substitutions: Arg for Lys-11 and Pro for
CC   Gly-31 (present sequence); Arg for Lys-11, Pro for Gly-31, and Gly for
CC   Pro-32 (see ABB79967); or Arg for Lys-11, Ser for Thr-12, Phe for His-13
CC   and Pro for Gly-31 (see ABB79969). These ELR-CXC chemokine antagonists
CC   are capable of binding to CXC receptors (CXCR1 or CXCR2) in mammalian
CC   inflammatory cells. The invention provides these novel ELR-CXC chemokine
CC   receptor antagonists, polynucleotides encoding them, vectors and host
CC   cells (bacteria, protozoa, yeast, fungi, algae, plant cells and animal
CC   cells) and viral hosts containing an expression vector, methods of
CC   production, and methods of using these for treating an ELR-CXC chemokine-
CC   mediated pathology in a bovid or a human, especially ischaemia-
CC   reperfusion injury, endotoxaemia-induced acute respiratory distress
CC   syndrome, immune complex-type glomerulonephritis, bacterial pneumonia, or
CC   mastitis, where the chemokine binds to CXCR1 or CXCR2 receptors (all
CC   claimed). Experimental results show that the present CXCL8(3-73)K11R/G31P
CC   protein competitively inhibits CXCL8 binding to neutrophils, does not
CC   display neutrophil agonist activity, blocks neutrophil chemotactic
CC   responses to both CXCR1 and CXCR2 ligands, is an effective in vitro
CC   antagonist of the neutrophil chemokines expressed in bacterial pneumonia
CC   or mastitis lesions, and is highly efficacious in blocking endotoxin-
CC   induced neutrophilic inflammation in vivo
XX
SQ   Sequence 72 AA;

  Query Match             100.0%;  Score 391;  DB 5;  Length 72;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-37;
  Matches   72;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TELRCQCIRTHSTPFHPKFIKELRVIESPPHCENSEIIVKLTNGNEVCLNPKEKWVQKVV 60
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Db          1 TELRCQCIRTHSTPFHPKFIKELRVIESPPHCENSEIIVKLTNGNEVCLNPKEKWVQKVV 60

Qy         61 QVFVKRAEKQDP 72
              ||||||||||||
Db         61 QVFVKRAEKQDP 72


RESULT 2
ABB79964
ID   ABB79964 standard; protein; 72 AA.
XX
AC   ABB79964;
XX
DT   19-DEC-2002  (first entry)
XX
DE   Bovine CXCL8(3-73)G31P, ELR-CXC chemokine receptor antagonist.
XX
KW   ELR-CXC; chemokine; receptor; antagonist; CXCL8; cattle;
KW   antiinflammatory; vasotropic; antibacterial; nephrotropic; mutant;
KW   mutein.
XX
OS   Bos taurus.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 29
FT                   /note= "wild-type Gly substituted by Pro"
XX
PN   WO200270565-A2.
XX
PD   12-SEP-2002.
XX
PF   01-MAR-2002; 2002WO-CA000271.
XX
PR   01-MAR-2001; 2001US-0273181P.
XX
PA   (UYSA-) UNIV SASKATCHEWAN TECHNOLOGIES INC.
XX
PI   Gordon JR,  Li F;
XX
DR   WPI; 2002-723251/78.
DR   N-PSDB; ABQ81432.
XX
PT   New ELR-CXC chemokine antagonist, useful for treating a CXC chemokine-
PT   mediated pathology, e.g. ischemia-reperfusion injury or endotoxemia-
PT   induced acute respiratory distress syndrome.
XX
PS   Disclosure; Page 57; 64pp; English.
XX
CC   The present sequence is the protein sequence of a mutated bovine bovine
CC   CXCL8 protein comprising amino acids 3-73 of the wild-type sequence with
CC   substitution of the native Gly-31 residue by Pro. Claimed ELR-CXC
CC   chemokine antagonists of the invention comprise an amino acid
CC   substantially equivalent to a wild-type bovine CXCL8 sequence, but having
CC   a truncation of the first 2 amino acid residues of bovine CXCL8, and
CC   having the following amino acid substitutions: Arg for Lys-11 and Pro for
CC   Gly-31 (see ABB79966); Arg for Lys-11, Pro for Gly-31, and Gly for Pro-32
CC   (see ABB79967); or Arg for Lys-11, Ser for Thr-12, Phe for His-13 and Pro
CC   for Gly-31 (see ABB79969). These ELR-CXC chemokine antagonists are
CC   capable of binding to CXC receptors (CXCR1 or CXCR2) in mammalian
CC   inflammatory cells. The invention provides these novel ELR-CXC chemokine
CC   receptor antagonists, polynucleotides encoding them, vectors and host
CC   cells (bacteria, protozoa, yeast, fungi, algae, plant cells and animal
CC   cells) and viral hosts containing an expression vector, methods of
CC   production, and methods of using these for treating an ELR-CXC chemokine-
CC   mediated pathology in a bovid or a human, especially ischaemia-
CC   reperfusion injury, endotoxaemia-induced acute respiratory distress
CC   syndrome, immune complex-type glomerulonephritis, bacterial pneumonia, or
CC   mastitis, where the chemokine binds to CXCR1 or CXCR2 receptors (all
CC   claimed). The present CXCL8(3-73)G31P protein is a highly effective
CC   antagonist of CXCL8 binding to cells
XX
SQ   Sequence 72 AA;

  Query Match             99.2%;  Score 388;  DB 5;  Length 72;
  Best Local Similarity   98.6%;  Pred. No. 4.9e-37;
  Matches   71;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          1 TELRCQCIKTHSTPFHPKFIKELRVIESPPHCENSEIIVKLTNGNEVCLNPKEKWVQKVV 60

Qy         61 QVFVKRAEKQDP 72
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Db         61 QVFVKRAEKQDP 72


RESULT 3
ABB79967
ID   ABB79967 standard; protein; 72 AA.
XX
AC   ABB79967;
XX
DT   19-DEC-2002  (first entry)
XX
DE   CXCL8(3-73)K11R/G31P/P32G, ELR-CXC chemokine receptor antagonist.
XX
KW   ELR-CXC; chemokine; receptor; antagonist; CXCL8; cattle;
KW   antiinflammatory; vasotropic; antibacterial; nephrotropic; mutant;
KW   mutein.
XX
OS   Bos taurus.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 9
FT                   /note= "wild-type Lys substituted by Arg"
FT   Misc-difference 29
FT                   /note= "wild-type Gly substituted by Pro"
FT   Misc-difference 30
FT                   /note= "wild-type Pro substituted by Gly"
XX
PN   WO200270565-A2.
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XX
PD 12-SEP-2002.
XX
PF 01-MAR-2002; 2002WO-CA000271.
XX
PR 01-MAR-2001; 2001US-0273181P.
XX
PA (UYSA-) UNIV SASKATCHEWAN TECHNOLOGIES INC.
XX
PI Gordon JR, Li F;
XX
DR WPI; 2002-723251/78.
DR N-PSDB; ABQ81435.
XX
PT New ELR-CXC chemokine antagonist, useful for treating a CXC chemokine-
PT mediated pathology, e.g. ischemia-reperfusion injury or endotoxemia-
PT induced acute respiratory distress syndrome.
XX
PS Disclosure; Page 62; 64pp; English.
XX
CC The present sequence is the protein sequence of a mutated bovine bovine
CC CXCL8 protein comprising amino acids 3-73 of the wild-type sequence with
CC substitution of the native Gly-31 amino acid residue by Pro, and
CC substitution of the native Lys-11 residue by Arg. Claimed ELR-CXC
CC chemokine antagonists of the invention comprise an amino acid
CC substantially equivalent to a wild-type bovine CXCL8 sequence, but having
CC a truncation of the first 2 amino acid residues of bovine CXCL8, and
CC having the following amino acid substitutions: Arg for Lys-11 and Pro for
CC Gly-31 (see ABB79966); Arg for Lys-11, Pro for Gly-31, and Gly for Pro-32
CC (present sequence); or Arg for Lys-11, Ser for Thr-12, Phe for His-13 and
CC Pro for Gly-31 (see ABB79969). These ELR-CXC chemokine antagonists are
CC capable of binding to CXC receptors (CXCR1 or CXCR2) in mammalian
CC inflammatory cells. The invention provides these novel ELR-CXC chemokine
CC receptor antagonists, polynucleotides encoding them, vectors and host
CC cells (bacteria, protozoa, yeast, fungi, algae, plant cells and animal
CC cells) and viral hosts containing an expression vector, methods of
CC production, and methods of using these for treating an ELR-CXC chemokine-
CC mediated pathology in a bovid or a human, especially ischaemia-
CC reperfusion injury, endotoxaemia-induced acute respiratory distress
CC syndrome, immune complex-type glomerulonephritis, bacterial pneumonia, or
CC mastitis, where the chemokine binds to CXCR1 or CXCR2 receptors (all
CC claimed)
XX
SQ Sequence 72 AA;

Query Match 97.7%; Score 382; DB 5; Length 72;
Best Local Similarity 98.6%; Pred. No. 2.4e-36;
Matches 71; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy         61 QVFVKRAEKQDP 72
              ||||||||||||
Db         61 QVFVKRAEKQDP 72
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RESULT 4
ABB79965
ID ABB79965 standard; protein; 72 AA.
XX
AC ABB79965;
XX
DT 19-DEC-2002 (first entry)
XX
DE Bovine CXCL8(3-73)K11R, ELR-CXC chemokine receptor antagonist.
XX
KW ELR-CXC; chemokine; receptor; antagonist; CXCL8; cattle;
KW antiinflammatory; vasotropic; antibacterial; nephrotropic; mutant;
KW mutein.
XX
OS Bos taurus.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 9
FT /note= "wild-type Lys substituted by Arg"
XX
PN WO200270565-A2.
XX
PD 12-SEP-2002.
XX
PF 01-MAR-2002; 2002WO-CA000271.
XX
PR 01-MAR-2001; 2001US-0273181P.
XX
PA (UYSA-) UNIV SASKATCHEWAN TECHNOLOGIES INC.
XX
PI Gordon JR, Li F;
XX
DR WPI; 2002-723251/78.
DR N-PSDB; ABQ81433.
XX
PT New ELR-CXC chemokine antagonist, useful for treating a CXC chemokine-
PT mediated pathology, e.g. ischemia-reperfusion injury or endotoxemia-
PT induced acute respiratory distress syndrome.
XX
PS Disclosure; Page 58; 64pp; English.
XX
CC The present sequence is the protein sequence of a mutated bovine bovine
CC CXCL8 protein comprising amino acids 3-73 of the wild-type sequence with
CC substitution of the native Lys-11 residue by Arg. Claimed ELR-CXC
CC chemokine antagonists of the invention comprise an amino acid
CC substantially equivalent to a wild-type bovine CXCL8 sequence, but having
CC a truncation of the first 2 amino acid residues of bovine CXCL8, and
CC having the following amino acid substitutions: Arg for Lys-11 and Pro for
CC Gly-31 (see ABB79966); Arg for Lys-11, Pro for Gly-31, and Gly for Pro-32
CC (see ABB79967); or Arg for Lys-11, Ser for Thr-12, Phe for His-13 and Pro
CC for Gly-31 (see ABB79969). These ELR-CXC chemokine antagonists are
CC capable of binding to CXC receptors (CXCR1 or CXCR2) in mammalian
CC inflammatory cells. The invention provides these novel ELR-CXC chemokine
CC receptor antagonists, polynucleotides encoding them, vectors and host
CC cells (bacteria, protozoa, yeast, fungi, algae, plant cells and animal
CC cells) and viral hosts containing an expression vector, methods of
CC production, and methods of using these for treating an ELR-CXC chemokine-
CC mediated pathology in a bovid or a human, especially ischaemia-
CC reperfusion injury, endotoxaemia-induced acute respiratory distress
CC syndrome, immune complex-type glomerulonephritis, bacterial pneumonia, or
CC mastitis, where the chemokine binds to CXCR1 or CXCR2 receptors (all
CC claimed)
XX
SQ Sequence 72 AA;

Query Match 97.7%; Score 382; DB 5; Length 72;
Best Local Similarity 98.6%; Pred. No. 2.4e-36;
Matches 71; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db          1 TELRCQCIRTHSTPFHPKFIKELRVIESGPHCENSEIIVKLTNGNEVCLNPKEKWVQKVV 60

Qy         61 QVFVKRAEKQDP 72
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Db         61 QVFVKRAEKQDP 72
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RESULT 5
ABB79969
ID ABB79969 standard; protein; 72 AA.
XX
AC ABB79969;
XX
DT 19-DEC-2002 (first entry)
XX
DE CXCL8(3-73)K11R/T12S/H13F/G31P, CXC chemokine receptor antagonist.

```
XX
KW   ELR-CXC; chemokine; receptor; antagonist; CXCL8; cattle;
KW   antiinflammatory; vasotropic; antibacterial; nephrotropic; mutant;
KW   mutein.
XX
OS   Bos taurus.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 9
FT                   /note= "wild-type Lys substituted by Arg"
FT   Misc-difference 10
FT                   /note= "wild-type Thr substituted by Ser"
FT   Misc-difference 11
FT                   /note= "wild-type His substituted by Phe"
FT   Misc-difference 29
FT                   /note= "wild-type Gly substituted by Pro"
XX
PN   WO200270565-A2.
XX
PD   12-SEP-2002.
XX
PF   01-MAR-2002; 2002WO-CA000271.
XX
PR   01-MAR-2001; 2001US-0273181P.
XX
PA   (UYSA-) UNIV SASKATCHEWAN TECHNOLOGIES INC.
XX
PI   Gordon JR,  Li F;
XX
DR   WPI; 2002-723251/78.
XX
PT   New ELR-CXC chemokine antagonist, useful for treating a CXC chemokine-
PT   mediated pathology, e.g. ischemia-reperfusion injury or endotoxemia-
PT   induced acute respiratory distress syndrome.
XX
PS   Disclosure; Page; 64pp; English.
XX
CC   The present sequence is the protein sequence of a mutated bovine bovine
CC   CXCL8 protein comprising amino acids 3-73 of the wild-type sequence with
CC   substitution of the native Lys-11 residue by Arg, native Thr-12 by Ser,
CC   native His-13 by Phe, and native Gly-31 by Pro. Claimed ELR-CXC chemokine
CC   antagonists of the invention comprise an amino acid substantially
CC   equivalent to a wild-type bovine CXCL8 sequence, but having a truncation
CC   of the first 2 amino acid residues of bovine CXCL8, and having the
CC   following amino acid substitutions: Arg for Lys-11 and Pro for Gly-31
CC   (see ABB79966); Arg for Lys-11, Pro for Gly-31, and Gly for Pro-32 (see
CC   ABB79967); or Arg for Lys-11, Ser for Thr-12, Phe for His-13 and Pro for
CC   Gly-31 (present sequence). The ELR-CXC chemokine antagonists are capable
CC   of binding to CXC receptors (CXCR1 or CXCR2) in mammalian inflammatory
CC   cells. The invention provides these novel ELR-CXC chemokine receptor
CC   antagonists, polynucleotides encoding them, vectors and host cells
CC   (bacteria, protozoa, yeast, fungi, algae, plant cells and animal cells)
CC   and viral hosts containing an expression vector, methods of production,
CC   and methods of using these for treating an ELR-CXC chemokine-mediated
CC   pathology in a bovid or a human, especially ischaemia-reperfusion injury,
CC   endotoxaemia-induced acute respiratory distress syndrome, immune complex-
CC   type glomerulonephritis, bacterial pneumonia, or mastitis, where the
CC   chemokine binds to CXCR1 or CXCR2 receptors (all claimed). Experimental
CC   results showed that amino acid substitutions at Thr-12 and His-13
CC   substantially reduced the antagonist activities of CXCL8(3-73)K11R/G31P.
CC   Note: The present sequence is not shown in the specification but is
CC   derived from the bovine CXCL8(3-73)K11R/G31P mutant sequence given in the
CC   Sequence Listing (see ABB79966)
XX
SQ   Sequence 72 AA;

  Query Match             93.6%;  Score 366;  DB 5;  Length 72;
  Best Local Similarity   95.8%;  Pred. No. 1.7e-34;
  Matches   69;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TELRCQCIRTHSTPFHPKFIKELRVIESPPHCENSEIIVKLTNGNEVCLNPKEKWVQKVV 60
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Db          1 TELRCQCIRSFSTPFHPKFIKELRVIESPPHRENSEIIVKLTNGNEVCLNPKEKWVQKVV 60

Qy         61 QVFVKRAEKQDP 72
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Db         61 QVFVKRAEKQDP 72


RESULT 6
ABB79968
ID   ABB79968 standard; protein; 72 AA.
XX
AC   ABB79968;
XX
DT   19-DEC-2002  (first entry)
XX
DE   CXCL8(3-73)K11R/T12S/H13F, ELR-CXC chemokine receptor antagonist.
XX
KW   ELR-CXC; chemokine; receptor; antagonist; CXCL8; cattle;
KW   antiinflammatory; vasotropic; antibacterial; nephrotropic; mutant;
KW   mutein.
XX
OS   Bos taurus.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 9
FT                   /note= "wild-type Lys substituted by Arg"
FT   Misc-difference 10
FT                   /note= "wild-type Thr substituted by Ser"
FT   Misc-difference 11
FT                   /note= "wild-type His substituted by Phe"
XX
PN   WO200270565-A2.
XX
PD   12-SEP-2002.
XX
PF   01-MAR-2002; 2002WO-CA000271.
XX
PR   01-MAR-2001; 2001US-0273181P.
XX
PA   (UYSA-) UNIV SASKATCHEWAN TECHNOLOGIES INC.
XX
PI   Gordon JR,  Li F;
XX
DR   WPI; 2002-723251/78.
DR   N-PSDB; ABQ81436.
XX
PT   New ELR-CXC chemokine antagonist, useful for treating a CXC chemokine-
PT   mediated pathology, e.g. ischemia-reperfusion injury or endotoxemia-
PT   induced acute respiratory distress syndrome.
XX
PS   Disclosure; Page 63-64; 64pp; English.
XX
CC   The present sequence is the protein sequence of a mutated bovine bovine
CC   CXCL8 protein comprising amino acids 3-73 of the wild-type sequence with
CC   substitution of the native Lys-11 residue by Arg, the native Thr-12
CC   residue by Ser, and the native His-13 residue by Phe. Claimed ELR-CXC
CC   chemokine antagonists of the invention comprise an amino acid
CC   substantially equivalent to a wild-type bovine CXCL8 sequence, but having
CC   a truncation of the first 2 amino acid residues of bovine CXCL8, and
CC   having the following amino acid substitutions: Arg for Lys-11 and Pro for
CC   Gly-31 (see ABB79966); Arg for Lys-11, Pro for Gly-31, and Gly for Pro-32
CC   (see ABB79967); or Arg for Lys-11, Ser for Thr-12, Phe for His-13 and Pro
CC   for Gly-31 (see ABB79969). These ELR-CXC chemokine antagonists are
CC   capable of binding to CXC receptors (CXCR1 or CXCR2) in mammalian
CC   inflammatory cells. The invention provides these novel ELR-CXC chemokine
CC   receptor antagonists, polynucleotides encoding them, vectors and host
CC   cells (bacteria, protozoa, yeast, fungi, algae, plant cells and animal
CC   cells) and viral hosts containing an expression vector, methods of
CC   production, and methods of using these for treating an ELR-CXC chemokine-
CC   mediated pathology in a bovid or a human, especially ischaemia-
CC   reperfusion injury, endotoxaemia-induced acute respiratory distress
CC   syndrome, immune complex-type glomerulonephritis, bacterial pneumonia, or
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CC   mastitis, where the chemokine binds to CXCR1 or CXCR2 receptors (all
CC   claimed). Experimental results showed that amino acid substitutions at
CC   Thr-12 and His-13 substantially reduced the antagonist activities of
CC   CXCL8(3-73)K11R/G31P
XX
SQ   Sequence 72 AA;

  Query Match             91.3%;  Score 357;  DB 5;  Length 72;
  Best Local Similarity   94.4%;  Pred. No. 1.8e-33;
  Matches   68;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 TELRCQCIRTHSTPFHPKFIKELRVIESPPHCENSEIIVKLTNGNEVCLNPKEKWVQKVV 60
              |||||||||: |||||||||||||||||| || ||||||||||||||||||||||||||||
Db          1 TELRCQCIRSFSTPFHPKFIKELRVIESGPHRENSEIIVKLTNGNEVCLNPKEKWVQKVV 60

Qy         61 QVFVKRAEKQDP 72
              ||||||||||||
Db         61 QVFVKRAEKQDP 72


RESULT 7
AAB07714
ID   AAB07714 standard; protein; 103 AA.
XX
AC   AAB07714;
XX
DT   07-NOV-2000  (first entry)
XX
DE   Amino acid sequence of porcine interleukin-8 (IL-8).
XX
KW   Neutrophil activating peptide 2; NAP-2; bone growth; bone stimulatory;
KW   bone apposition; bone reduction disease; osteoporosis; interleukin-8;
KW   IL-8.
XX
OS   Sus sp.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 51
FT                   /note= "unspecified amino acid given as Gle"
FT   Misc-difference 56
FT                   /note= "unspecified amino acid given as Gle"
XX
PN   WO200042069-A1.
XX
PD   20-JUL-2000.
XX
PF   13-JAN-2000; 2000WO-CA000031.
XX
PR   13-JAN-1999;   99US-00229304.
XX
PA   (OSTE-) OSTEOPHARM INC.
XX
PI   Tam CS;
XX
DR   WPI; 2000-466127/40.
XX
PT   Polypeptide comprising a fragment of a neutrophil-activating peptide
PT   variant is used for promoting bone growth and treating osteoporosis.
XX
PS   Disclosure; Page 30; 35pp; English.
XX
CC   The present sequence represents a porcine interleukin-8 (IL-8). IL-8 and
CC   neutrophil activating peptide 2 (NAP-2) are alpha-chemokines. The
CC   specification describes a polypeptide which promotes bone growth in
CC   mammals, and contains subsequences of variants of NAP-2. The polypeptide
CC   has bone stimulatory activity, and increases bone apposition rate. The
CC   polypeptide is used in the prevention and treatment of a bone reduction
CC   related disease. It is used for promoting bone growth and increasing bone
CC   growth, especially to treat osteoporosis. Antibodies against the
CC   polypeptide could be used to determine the presence of the polypeptides
CC   in blood serum to find subjects which are deficient in the polypeptide
XX
SQ   Sequence 103 AA;

  Query Match             79.8%;  Score 312;  DB 3;  Length 103;
  Best Local Similarity   84.1%;  Pred. No. 4.4e-28;
  Matches   58;  Conservative    3;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          2 ELRCQCIRTHSTPFHPKFIKELRVIESPPHCENSEIIVKLTNGNEVCLNPKEKWVQKVVQ 61
              ||||||| |||||||||||| |||| |  |||||||||| || ||||:||||||||||||
Db         31 ELRCQCINTHSTPFHPKFIKXLRVIXSGFHCENSEIIVKLVNGKEVCLDPKEKWVQKVVQ 90

Qy         62 VFVKRAEKQ 70
              :|:|| |||
Db         91 IFLKRTEKQ 99


RESULT 8
AAB86153
ID   AAB86153 standard; protein; 72 AA.
XX
AC   AAB86153;
XX
DT   31-JUL-2001  (first entry)
XX
DE   Human interleukin-8 mutant Y13H protein.
XX
KW   Interleukin-8; IL-8; human; mutant; mutein; alpha-factor signal sequence;
KW   fusion construct; anticancer; cancer treatment; CXCR1 receptor;
KW   CXCR2 receptor.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   DE19952622-A1.
XX
PD   10-MAY-2001.
XX
PF   02-NOV-1999;   99DE-01052622.
XX
PR   02-NOV-1999;   99DE-01052622.
XX
PA   (FARB ) BAYER AG.
XX
PI   Apeler H,  Schneider K,  Gottschalk U,  Schroeder W;
XX
DR   WPI; 2001-309395/33.
DR   N-PSDB; AAH20503.
XX
PT   Preparing correctly processed interleukin-8, or muteins, useful as
PT   anticancer agents, by expression in yeast as fusion with alpha-factor
PT   signal sequence.
XX
PS   Example 3; Page 13; 14pp; German.
XX
CC   This invention describes a novel preparation of correctly processed
CC   interleukin-8 (IL-8), or its muteins, by expressing them as fusions with
CC   the alpha-factor signal sequence (A) in yeast, with subsequent
CC   purification by ion-exchange and reverse-phase chromatography. The
CC   products of the invention have anticancer activity and can be used in a
CC   method to produce IL-8 muteins that are useful for (i) treatment of
CC   cancer and (ii) for identifying IL-8 antagonists, active at the CXCR1 and
CC   CXCR2 receptors. When expressed as a fusion with (A), IL-8 or its muteins
CC   are produced in high yield, free from endotoxins and with the correct N-
CC   terminus. The method is suitable for large scale production. This
CC   sequence represents the human mutant IL-8, Y13H which is used in the
CC   method described in the invention
XX
SQ   Sequence 72 AA;

  Query Match             74.9%;  Score 293;  DB 4;  Length 72;
  Best Local Similarity   77.6%;  Pred. No. 4.5e-26;
  Matches   52;  Conservative    9;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          2 ELRCQCIRTHSTPFHPKFIKELRVIESPPHCENSEIIVKLTNGNEVCLNPKEKWVQKVVQ 61
              |||||||:||| |||||||||||||| ||| |:|||||::| |:||:||| |||:||:
```

```
Db          4 ELRCQCIKTHSKPFHPKFIKELRVIESGPHCANTEIIVKLSDGRELCLDPKENWVQRVVE 63

Qy         62 VFVKRAE 68
              |:||||
Db         64 KFLKRAE 70


RESULT 9
AAW25706
ID   AAW25706 standard; protein; 72 AA.
XX
AC   AAW25706;
XX
DT   17-OCT-1997  (first entry)
XX
DE   Mutant human IL-8, R47K,D52N.
XX
KW   Interleukin-8; IL-8; IL-8 receptor-mediated biological response; mutant;
KW   IL-8 receptor; overlap PCR.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 47
FT                   /label= R47K
FT   Misc-difference 52
FT                   /label= D52N
XX
PN   WO9700601-A2.
XX
PD   09-JAN-1997.
XX
PF   18-JUN-1996;   96WO-US010537.
XX
PR   20-JUN-1995;   95US-0002774P.
PR   18-OCT-1995;   95US-0005385P.
PR   05-APR-1996;   96US-00628455.
XX
PA   (CHIR ) CHIRON CORP.
XX
PI   Wernette-Hammond ME,  Shyamala V,  Siani M,  Blaney J;
PI   Tekamp-Olson P;
XX
DR   WPI; 1997-087095/08.
XX
PT   New mutant interleukin-8 poly:peptide(s) - used for modulating
PT   interleukin-8 receptor-mediated biological responses.
XX
PS   Claim 1; Page 34; 40pp; English.
XX
CC   The sequences given in AAW25701-14 represent interleukin-8 (IL-8) mutants
CC   which are capable of binding to IL-8 receptors. They can be used for
CC   modulating an IL-8 receptor-mediated biological response. The mutations
CC   were introduced into the human IL-8 coding sequence by overlap PCR
XX
SQ   Sequence 72 AA;

  Query Match             74.7%;  Score 292;  DB 2;  Length 72;
  Best Local Similarity   77.6%;  Pred. No. 5.9e-26;
  Matches   52;  Conservative    9;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          2 ELRCQCIRTHSTPFHPKFIKELRVIESPPHCENSEIIVKLTNGNEVCLNPKEKWVQKVVQ 61
              ||||||:|:| |||||||||||||| ||| |:||||||::| |:||||| |||:||:
Db          4 ELRCQCIKTYSKPFHPKFIKELRVIESGPHCANTEIIVKLSDGKELCLNPKENWVQRVVE 63

Qy         62 VFVKRAE 68
              |:||||
Db         64 KFLKRAE 70


RESULT 10
AAR38081
ID   AAR38081 standard; protein; 69 AA.
XX
AC   AAR38081;
XX
DT   25-MAR-2003  (revised)
DT   13-OCT-1993  (first entry)
XX
DE   Modified human interleukin-8 analogue (4-72).
XX
KW   Analogues; modified; neutrophil activators; antagonists; human;
KW   competitive antagonist; IL-8; inflammation; treatment; chemotaxis;
KW   activity; stimulation; inflammatory response.
XX
OS   Synthetic.
XX
PN   WO9311159-A1.
XX
PD   10-JUN-1993.
XX
PF   03-DEC-1992;   92WO-CA000528.
XX
PR   04-DEC-1991;   91US-00801578.
XX
PA   (BIOM-) BIOMEDICAL RES CENT LTD.
XX
PI   Clark-Lewis I,  Moser B;
XX
DR   WPI; 1993-196997/24.
XX
PT   New interleukin-8 analogues modified in specified region - used as
PT   neutrophil activators or for blocking effect of IL-8 on neutrophil(s),
PT   for treatment of inflammation.
XX
PS   Claim 9; Page 29; 47pp; English.
XX
CC   The sequence is that of an analogue of interleukin-8 (IL-8) comprising IL
CC   -8 residues 4-72. It is able to bind neutrophils and act as a competitive
CC   antagonist of IL-8, i.e. it can be used to treat inflammation, e.g. by
CC   intravenous injection or oral admin. It can act as a neutrophil activator
CC   and so can be used to stimulate an inflammatory response. (Updated on 25-
CC   MAR-2003 to correct PN field.)
XX
SQ   Sequence 69 AA;

  Query Match             74.2%;  Score 290;  DB 2;  Length 69;
  Best Local Similarity   77.6%;  Pred. No. 9.5e-26;
  Matches   52;  Conservative    9;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          2 ELRCQCIRTHSTPFHPKFIKELRVIESPPHCENSEIIVKLTNGNEVCLNPKEKWVQKVVQ 61
              ||||||:|:| |||||||||||||| ||| |:||||||::| |:||||| |||:||:
Db          1 ELRCQCIKTYSKPFHPKFIKELRVIESGPHCANTEIIVKLSDGRELCLDPKENWVQRVVQ 60

Qy         62 VFVKRAE 68
              |:||||
Db         61 KFLKRAE 67


RESULT 11
AAR38080
ID   AAR38080 standard; protein; 72 AA.
XX
AC   AAR38080;
XX
DT   25-MAR-2003  (revised)
DT   13-OCT-1993  (first entry)
XX
DE   Human interleukin-8 monomer.
XX
KW   Analogues; modified; neutrophil activators; antagonists; IL-8.
XX
OS   Homo sapiens.
XX
PN   WO9311159-A1.
XX
```

PD 10-JUN-1993.
XX
PF 03-DEC-1992; 92WO-CA000528.
XX
PR 04-DEC-1991; 91US-00801578.
XX
PA (BIOM-) BIOMEDICAL RES CENT LTD.
XX
PI Clark-Lewis I, Moser B;
XX
DR WPI; 1993-196997/24.
XX
PT New interleukin-8 analogues modified in specified region - used as
PT neutrophil activators or for blocking effect of IL-8 on neutrophil(s),
PT for treatment of inflammation.
XX
PS Disclosure; Page 8; 47pp; English.
XX
CC The sequence is that of the 72-residue form of the interleukin (IL-8)
CC monomer. It may be modified to produce biologically active analogues of
CC IL-8 which are able to bind neutrophils and act as competitive
CC antagonists of IL-8, i.e. they can be used to treat inflammation.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 72 AA;

Query Match 74.2%; Score 290; DB 2; Length 72;
Best Local Similarity 77.6%; Pred. No. 1e-25;
Matches 52; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

```
Qy          2 ELRCQCIRTHSTPFHPKFIKELRVIESPPHCENSEIIVKLTNGNEVCLNPKEKWVQKVVQ 61
              ||||||:|:| |||||||||||||| ||| |:||||||::| |:||:||| |||:||| 
Db          4 ELRCQCIKTYSKPFHPKFIKELRVIESGPHCANTEIIVKLSDGRELCLDPKENWVQRVVQ 63

Qy         62 VFVKRAE 68
                |:||||
Db         64 KFLKRAE 70
```

RESULT 12
AAW25704
ID AAW25704 standard; protein; 72 AA.
XX
AC AAW25704;
XX
DT 17-OCT-1997 (first entry)
XX
DE Mutant human IL-8, E48K,D52N.
XX
KW Interleukin-8; IL-8; IL-8 receptor-mediated biological response; mutant;
KW IL-8 receptor; overlap PCR.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 48
FT /label= E48K
FT Misc-difference 52
FT /label= D52N
XX
PN WO9700601-A2.
XX
PD 09-JAN-1997.
XX
PF 18-JUN-1996; 96WO-US010537.
XX
PR 20-JUN-1995; 95US-0002774P.
PR 18-OCT-1995; 95US-0005385P.
PR 05-APR-1996; 96US-00628455.
XX
PA (CHIR) CHIRON CORP.
XX
PI Wernette-Hammond ME, Shyamala V, Siani M, Blaney J;
PI Tekamp-Olson P;
XX
DR WPI; 1997-087095/08.
XX
PT New mutant interleukin-8 poly:peptide(s) - used for modulating
PT interleukin-8 receptor-mediated biological responses.
XX
PS Claim 1; Page 34; 40pp; English.
XX
CC The sequences given in AAW25701-14 represent interleukin-8 (IL-8) mutants
CC which are capable of binding to IL-8 receptors. They can be used for
CC modulating an IL-8 receptor-mediated biological response. The mutations
CC were introduced into the human IL-8 coding sequence by overlap PCR
XX
SQ Sequence 72 AA;

Query Match 73.7%; Score 288; DB 2; Length 72;
Best Local Similarity 76.1%; Pred. No. 1.7e-25;
Matches 51; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

```
Qy          2 ELRCQCIRTHSTPFHPKFIKELRVIESPPHCENSEIIVKLTNGNEVCLNPKEKWVQKVVQ 61
              ||||||:|:| |||||||||||||| ||| |:||||||::| ::|||||| |||:||: 
Db          4 ELRCQCIKTYSKPFHPKFIKELRVIESGPHCANTEIIVKLSDGRKLCLNPKENWVQRVVE 63

Qy         62 VFVKRAE 68
                |:||||
Db         64 KFLKRAE 70
```

RESULT 13
AAW25705
ID AAW25705 standard; protein; 72 AA.
XX
AC AAW25705;
XX
DT 17-OCT-1997 (first entry)
XX
DE Mutant human IL-8, R47K,E48K,D52N.
XX
KW Interleukin-8; IL-8; IL-8 receptor-mediated biological response; mutant;
KW IL-8 receptor; overlap PCR.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 47
FT /label= R47K
FT Misc-difference 48
FT /label= E48K
FT Misc-difference 52
FT /label= D52N
XX
PN WO9700601-A2.
XX
PD 09-JAN-1997.
XX
PF 18-JUN-1996; 96WO-US010537.
XX
PR 20-JUN-1995; 95US-0002774P.
PR 18-OCT-1995; 95US-0005385P.
PR 05-APR-1996; 96US-00628455.
XX
PA (CHIR) CHIRON CORP.
XX
PI Wernette-Hammond ME, Shyamala V, Siani M, Blaney J;
PI Tekamp-Olson P;
XX
DR WPI; 1997-087095/08.
XX
PT New mutant interleukin-8 poly:peptide(s) - used for modulating
PT interleukin-8 receptor-mediated biological responses.
XX
PS Claim 1; Page 34; 40pp; English.

```
XX
CC   The sequences given in AAW25701-14 represent interleukin-8 (IL-8) mutants
CC   which are capable of binding to IL-8 receptors. They can be used for
CC   modulating an IL-8 receptor-mediated biological response. The mutations
CC   were introduced into the human IL-8 coding sequence by overlap PCR
XX
SQ   Sequence 72 AA;

  Query Match             73.7%;  Score 288;  DB 2;  Length 72;
  Best Local Similarity   76.1%;  Pred. No. 1.7e-25;
  Matches   51;  Conservative   10;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          2 ELRCQCIRTHSTPFHPKFIKELRVIESPPHCENSEIIVKLTNGNEVCLNPKEKWVQKVVQ 61
              |||||||:|:| |||||||||||||| ||| |:||||||::| ::|||||| |||:||:
Db          4 ELRCQCIKTYSKPFHPKFIKELRVIESGPHCANTEIIVKLSDGKKLCLNPKENWVQRVVE 63

Qy         62 VFVKRAE 68
                |:||||
Db         64 KFLKRAE 70


RESULT 14
ABG30773
ID   ABG30773 standard; protein; 71 AA.
XX
AC   ABG30773;
XX
DT   05-NOV-2002  (first entry)
XX
DE   1ILP complex polypeptide structure.
XX
KW   Cytokine; immune disorder; autoimmune disease; 1ILP; interleukin 8; IL-8;
KW   inflammatory disorder; allergy; rhinitis; neoplastic disorder; tumour;
KW   haematological disease; myeloproliferative disorder; Hodgkin's disease;
KW   osteoporosis; obesity; diabetes; gout; cardiovascular disorder; AIDS;
KW   reperfusion injury; atherosclerosis; ischaemic heart disease; stroke;
KW   cardiac failure; liver disease; neurological disorder; male infertility;
KW   acquired immunodeficiency syndrome; ageing; bacterial infection; cancer;
KW   viral infection; cytomegalovirus.
XX
OS   Unidentified.
XX
PN   WO200229062-A2.
XX
PD   11-APR-2002.
XX
PF   04-OCT-2001; 2001WO-GB004412.
XX
PR   04-OCT-2000; 2000GB-00024283.
XX
PA   (IMPH-) IMPHARMATICA LTD.
XX
PI   Fagan RJ,  Phelps CB,  Gutteridge A;
XX
DR   WPI; 2002-590419/63.
XX
PT   Novel cytokine polypeptides useful for treating immune disorders e.g.
PT   autoimmune disease, rheumatoid arthritis, osteoarthritis, inflammatory
PT   disorders, dermatological disease, neoplastic disorders and AIDS.
XX
PS   Example 1; Fig 8; 86pp; English.
XX
CC   The invention relates to a cytokine polypeptide (CC1 or CC2), termed
CC   AAA85885.1 and AAA85894.1, and its associated polynucleotide. The
CC   sequences are useful for the treatment of a disease selected from immune
CC   disorders such as autoimmune disease, rheumatoid arthritis,
CC   osteoarthritis, psoriasis, systemic lupus erythematosus, and multiple
CC   sclerosis, inflammatory disorders such as allergy, rhinitis,
CC   conjunctivitis, glomerulonephritis, uveitis, Crohn's disease, ulcerative
CC   colitis, inflammatory bowel disease, pancreatitis, digestive system
CC   inflammation, sepsis, endotoxic shock, septic shock, cachexia, myalgia,
CC   ankylosing spondylitis, myasthenia gravis, post-viral fatigue syndrome,
CC   pulmonary disease, respiratory distress syndrome, asthma, wound healing,
CC   chronic-obstructive pulmonary disease, airway inflammation,
CC   endometriosis, dermatological disease, Behcet's disease, neoplastic
CC   disorders such as melanoma, sarcoma, renal tumour, colon tumour,
CC   haematological disease, myeloproliferative disorder, Hodgkin's disease,
CC   osteoporosis, obesity, diabetes, gout, cardiovascular disorders,
CC   reperfusion injury, atherosclerosis, ischaemic heart disease, cardiac
CC   failure, stroke, liver disease, AIDS, AIDS related complex, neurological
CC   disorders, male infertility, ageing and bacterial infections including
CC   Plasmodium infection or viral infection, particularly human herpesvirus 5
CC   (cytomegalovirus) infection. This sequence represents an interleukin 8
CC   (IL-8) dimer in complex with a fragment of the IL-8 receptor, used in the
CC   scope of the invention. The complex structure is termed the 1ILP
CC   polypeptide
XX
SQ   Sequence 71 AA;

  Query Match             73.4%;  Score 287;  DB 5;  Length 71;
  Best Local Similarity   76.1%;  Pred. No. 2.2e-25;
  Matches   51;  Conservative   10;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          2 ELRCQCIRTHSTPFHPKFIKELRVIESPPHCENSEIIVKLTNGNEVCLNPKEKWVQKVVQ 61
              |||||||:|:| |||||||||||||| ||| |:||||||::| |:||:||| |||:||:
Db          3 ELRCQCIKTYSKPFHPKFIKELRVIESGPHCANTEIIVKLSDGRELCLDPKENWVQRVVE 62

Qy         62 VFVKRAE 68
                |:||||
Db         63 KFLKRAE 69


RESULT 15
AAP81838
ID   AAP81838 standard; peptide; 72 AA.
XX
AC   AAP81838;
XX
DT   25-MAR-2003  (revised)
DT   10-MAR-2003  (revised)
DT   17-DEC-2001  (revised)
DT   07-NOV-1990  (first entry)
XX
DE   Sequence of a synthetic neutrophil chemotactic polypeptide (NCF).
XX
KW   Inflammation; anti-neutrophil chemotactic polypeptide antibody.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   USN7169033-N.
XX
PD   27-SEP-1988.
XX
PF   16-MAR-1988;   88US-00169033.
XX
PR   16-MAR-1988;   88US-00169033.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICE.
PA   (USDC ) US SEC OF COMMERCE.
XX
PI   Matsushima K,  Yoshimur T,  Leonard EJ,  Oppenheime J,  Appella E;
XX
DR   WPI; 1988-322571/45.
XX
PT   Synthetic neutrophil chemo:tactic factor - and its monoclonal antibodies
PT   useful for treating inflammatory conditions.
XX
PS   Claim 1; Page 8; 11pp; English.
XX
CC   The claimed NCF is composed in whole or in part of the AA sequence in
CC   AAP90913. Anti-NCF MAbs are useful for treating inflammatory conditions.
CC   (Note: Revised entry submitted to correct the patent number format of US
CC   Government-owned NTIS applications to prevent clashes with ongoing US
CC   granted patent numbers. For further information please visit the Derwent
CC   web site at www.derwent.com/dwpi/updates/ntis_us.html.) (Updated on 10-
```

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CC   MAR-2003 to add missing OS field.) (Updated on 25-MAR-2003 to correct PA
CC   field.) (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ   Sequence 72 AA;

  Query Match             73.4%;  Score 287;  DB 1;  Length 72;
  Best Local Similarity   76.1%;  Pred. No. 2.2e-25;
  Matches   51;  Conservative   10;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          2 ELRCQCIRTHSTPFHPKFIKELRVIESPPHCENSEIIVKLTNGNEVCLNPKEKWVQKVVQ 61
              ||||||:|:| |||||||||||||| ||| |:||||||::| |:||:||| |||:||:
Db          4 ELRCQCIKTYSKPFHPKFIKELRVIESGPHCANTEIIVKLSDGRELCLDPKENWVQRVVE 63

Qy         62 VFVKRAE 68
                |:||||
Db         64 KFLKRAE 70


Search completed: December 13, 2004, 19:49:13
Job time : 153 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: December 13, 2004, 19:52:49 ; Search time 144 Seconds
(without alignments)
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Gapop 10.0 , Gapext 0.5

Searched: 1585576 seqs, 357178320 residues

Total number of hits satisfying chosen parameters: 1585576

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
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15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	391	100.0	72	14	US-10-087-273-1	Sequence 1, Appli
2	379	96.9	74	14	US-10-087-273-2	Sequence 2, Appli
3	324	82.9	103	9	US-09-229-304-9	Sequence 9, Appli
4	287	73.4	72	10	US-09-811-162-5	Sequence 5, Appli
5	287	73.4	72	13	US-10-037-218A-2	Sequence 2, Appli
6	287	73.4	72	16	US-10-668-733-13	Sequence 13, Appl
7	287	73.4	72	16	US-10-668-733-18	Sequence 18, Appl
8	287	73.4	72	16	US-10-803-960-16	Sequence 16, Appl
9	287	73.4	73	14	US-10-207-330-26	Sequence 26, Appl
10	287	73.4	76	14	US-10-104-755-79	Sequence 79, Appl
11	287	73.4	77	9	US-09-792-793A-19	Sequence 19, Appl
12	287	73.4	77	10	US-09-811-162-4	Sequence 4, Appli
13	287	73.4	77	14	US-10-375-209A-19	Sequence 19, Appl
14	287	73.4	77	15	US-10-332-038A-22	Sequence 22, Appl
15	287	73.4	77	17	US-10-243-795-1	Sequence 1, Appli
16	287	73.4	79	9	US-09-229-304-8	Sequence 8, Appli
17	287	73.4	99	8	US-08-927-939-23	Sequence 23, Appl
18	287	73.4	99	9	US-09-981-353-175	Sequence 175, App
19	287	73.4	99	13	US-10-121-119-3	Sequence 3, Appli
20	287	73.4	99	14	US-10-099-007A-4	Sequence 4, Appli
21	287	73.4	99	14	US-10-104-755-3	Sequence 3, Appli
22	287	73.4	99	14	US-10-171-311-93	Sequence 93, Appl
23	287	73.4	99	14	US-10-235-994-6	Sequence 6, Appli
24	287	73.4	99	14	US-10-301-822-87	Sequence 87, Appl
25	287	73.4	99	14	US-10-170-385-251	Sequence 251, App
26	287	73.4	99	14	US-10-295-027-187	Sequence 187, App
27	287	73.4	99	14	US-10-295-027-1209	Sequence 1209, Ap
28	287	73.4	99	15	US-10-440-464-183	Sequence 183, App
29	287	73.4	99	15	US-10-188-832-62	Sequence 62, Appl
30	287	73.4	99	16	US-10-734-564-74	Sequence 74, Appl
31	287	73.4	99	17	US-10-733-878-511	Sequence 511, App
32	280	71.6	76	14	US-10-104-755-83	Sequence 83, Appl
33	279	71.4	76	14	US-10-104-755-81	Sequence 81, Appl
34	263	67.3	91	9	US-09-755-665-48	Sequence 48, Appl
35	263	67.3	91	9	US-09-755-665-50	Sequence 50, Appl
36	263	67.3	91	16	US-10-629-248-48	Sequence 48, Appl
37	263	67.3	91	16	US-10-629-248-50	Sequence 50, Appl
38	193	49.4	86	10	US-09-811-162-2	Sequence 2, Appli
39	193	49.4	103	13	US-10-121-119-1	Sequence 1, Appli
40	179	45.8	98	15	US-10-115-479-24	Sequence 24, Appl
41	161.5	41.3	72	15	US-10-146-182-1	Sequence 1, Appli
42	161.5	41.3	96	10	US-09-771-023-9	Sequence 9, Appli
43	148.5	38.0	132	9	US-09-764-898-258	Sequence 258, App
44	148.5	38.0	132	9	US-09-764-903-53	Sequence 53, Appl
45	148.5	38.0	132	9	US-09-764-877-2055	Sequence 2055, Ap

ALIGNMENTS

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RESULT 1
US-10-087-273-1
; Sequence 1, Application US/10087273
; Publication No. US20030077705A1
; GENERAL INFORMATION:
;  APPLICANT: Gordon, John R.
;  APPLICANT:  Li, Fang
;  TITLE OF INVENTION: HIGH-AFFINITY ANTAGONISTS OF ELR-CXC CHEMOKINES
;  FILE REFERENCE: 47957
;  CURRENT APPLICATION NUMBER: US/10/087,273
;  CURRENT FILING DATE:  2002-08-23
;  PRIOR APPLICATION NUMBER: US 60/273,181
;  PRIOR FILING DATE: 2001-03-01
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 72
;   TYPE: PRT
;   ORGANISM: Bos taurus
US-10-087-273-1

  Query Match           100.0%;  Score 391;  DB 14;  Length 72;
  Best Local Similarity  100.0%;  Pred. No. 6.6e-38;
  Matches   72;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          1 TELRCQCIRTHSTPFHPKFIKELRVIESPPHCENSEIIVKLTNGNEVCLNPKEKWVQKVV 60

Qy         61 QVFVKRAEKQDP 72
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Db         61 QVFVKRAEKQDP 72


RESULT 2
US-10-087-273-2
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; Sequence 2, Application US/10087273
; Publication No. US20030077705A1
; GENERAL INFORMATION:
;  APPLICANT: Gordon, John R.
;  APPLICANT:  Li, Fang
;  TITLE OF INVENTION: HIGH-AFFINITY ANTAGONISTS OF ELR-CXC CHEMOKINES
;  FILE REFERENCE: 47957
;  CURRENT APPLICATION NUMBER: US/10/087,273
;  CURRENT FILING DATE:  2002-08-23
;  PRIOR APPLICATION NUMBER: US 60/273,181
;  PRIOR FILING DATE: 2001-03-01
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 74
;   TYPE: PRT
;   ORGANISM: Bos taurus
US-10-087-273-2

  Query Match             96.9%;  Score 379;  DB 14;  Length 74;
  Best Local Similarity   97.2%;  Pred. No. 1.7e-36;
  Matches   70;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TELRCQCIRTHSTPFHPKFIKELRVIESPPHCENSEIIVKLTNGNEVCLNPKEKWVQKVV 60
              ||||||||:|||||||||||||||||||| ||||||||||||||||||||||||||||||
Db          3 TELRCQCIKTHSTPFHPKFIKELRVIESGPHCENSEIIVKLTNGNEVCLNPKEKWVQKVV 62

Qy         61 QVFVKRAEKQDP 72
              ||||||||||||
Db         63 QVFVKRAEKQDP 74


RESULT 3
US-09-229-304-9
; Sequence 9, Application US/09229304
; Patent No. US20020090671A1
; GENERAL INFORMATION:
;  APPLICANT: TAM, Cherk Shing
;  TITLE OF INVENTION: BONE STIMULATING FACTOR
;  FILE REFERENCE: 079997/0123
;  CURRENT APPLICATION NUMBER: US/09/229,304
;  CURRENT FILING DATE: 1999-01-13
;  EARLIER APPLICATION NUMBER: US 09/048,058
;  EARLIER FILING DATE: 1998-03-26
;  EARLIER APPLICATION NUMBER: PCT/CA96/00653
;  EARLIER FILING DATE: 1996-09-26
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
;   LENGTH: 103
;   TYPE: PRT
;   ORGANISM: Porcine
US-09-229-304-9

  Query Match             82.9%;  Score 324;  DB 9;  Length 103;
  Best Local Similarity   87.0%;  Pred. No. 6.5e-30;
  Matches   60;  Conservative    3;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          2 ELRCQCIRTHSTPFHPKFIKELRVIESPPHCENSEIIVKLTNGNEVCLNPKEKWVQKVVQ 61
              ||||||| ||||||||||||||||||||  |||||||||| || ||||:|||||||||||
Db         31 ELRCQCINTHSTPFHPKFIKELRVIESGFHCENSEIIVKLVNGKEVCLDPKEKWVQKVVQ 90

Qy         62 VFVKRAEKQ 70
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Db         91 IFLKRTEKQ 99


RESULT 4
US-09-811-162-5
; Sequence 5, Application US/09811162
; Publication No. US20030040109A1
; GENERAL INFORMATION:
;  APPLICANT: Martins-Green, Manuela
;  APPLICANT:  Feugate, Jo Ellen
;  APPLICANT:  Li, QiJing
;  TITLE OF INVENTION: Chemokines and Methods for Inducing the Differentiation of Fibrob
;  TITLE OF INVENTION:  Myofibroblasts
;  FILE REFERENCE: 407E-000500US
;  CURRENT APPLICATION NUMBER: US/09/811,162
;  CURRENT FILING DATE:  2001-07-30
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
;   LENGTH: 72
;   TYPE: PRT
;   ORGANISM: Homosapiens
US-09-811-162-5

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  Best Local Similarity   76.1%;  Pred. No. 8.9e-26;
  Matches   51;  Conservative   10;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          2 ELRCQCIRTHSTPFHPKFIKELRVIESPPHCENSEIIVKLTNGNEVCLNPKEKWVQKVVQ 61
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Db          4 ELRCQCIKTYSKPFHPKFIKELRVIESGPHCANTEIIVKLSDGRELCLDPKENWVQRVVE 63

Qy         62 VFVKRAE 68
              |:||||
Db         64 KFLKRAE 70


RESULT 5
US-10-037-218A-2
; Sequence 2, Application US/10037218A
; Publication No. US20020151706A1
; GENERAL INFORMATION:
;  APPLICANT: Matsushima, Kouji
;  APPLICANT:  Yoshimura, Teizo
;  APPLICANT:  Leonard, Edward
;  APPLICANT:  Oppenhiem, Joost
;  APPLICANT:  Appella, Ettore
;  APPLICANT:  Showalter, Stephen
;  TITLE OF INVENTION: NOVEL NEUTROPHIL CHEMOTACTIC FACTOR, CLONED cDNA AND MONOCLONAL A
;  TITLE OF INVENTION:  THERETO
;  FILE REFERENCE: 2026-4052US4
;  CURRENT APPLICATION NUMBER: US/10/037,218A
;  CURRENT FILING DATE:  2001-11-09
;  PRIOR APPLICATION NUMBER: US 08/818,631
;  PRIOR FILING DATE: 1997-03-14
;  PRIOR APPLICATION NUMBER: US 07/169,033
;  PRIOR FILING DATE: 1988-03-16
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 72
;   TYPE: PRT
;   ORGANISM: homo sapiens
US-10-037-218A-2

  Query Match             73.4%;  Score 287;  DB 13;  Length 72;
  Best Local Similarity   76.1%;  Pred. No. 8.9e-26;
  Matches   51;  Conservative   10;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          2 ELRCQCIRTHSTPFHPKFIKELRVIESPPHCENSEIIVKLTNGNEVCLNPKEKWVQKVVQ 61
              |||||||:|:| |||||||||||||||| ||| |:||||||::| |:||:||| |||:||:
Db          4 ELRCQCIKTYSKPFHPKFIKELRVIESGPHCANTEIIVKLSDGRELCLDPKENWVQRVVE 63

Qy         62 VFVKRAE 68
              |:||||
Db         64 KFLKRAE 70


RESULT 6
US-10-668-733-13
; Sequence 13, Application US/10668733
; Publication No. US20040138422A1
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; GENERAL INFORMATION:
;  APPLICANT: Demotz et al.
;  TITLE OF INVENTION: SYNTHETIC CHEMOKINES LABELED AT SELECTED POSITIONS
;  FILE REFERENCE: 29964/38772A
;  CURRENT APPLICATION NUMBER: US/10/668,733
;  CURRENT FILING DATE:  2003-09-23
;  PRIOR APPLICATION NUMBER: US 60/412,866
;  PRIOR FILING DATE: 2002-09-23
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
;   LENGTH: 72
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic peptide
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (71)..(71)
;   OTHER INFORMATION: The amino acid at position 71 is Dpr(Ser) linked to AlexaFluor647
US-10-668-733-13

  Query Match             73.4%;  Score 287;  DB 16;  Length 72;
  Best Local Similarity   76.1%;  Pred. No. 8.9e-26;
  Matches   51;  Conservative   10;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          2 ELRCQCIRTHSTPFHPKFIKELRVIESPPHCENSEIIVKLTNGNEVCLNPKEKWVQKVVQ 61
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Qy         62 VFVKRAE 68
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Db         64 KFLKRAE 70


RESULT 7
US-10-668-733-18
; Sequence 18, Application US/10668733
; Publication No. US20040138422A1
; GENERAL INFORMATION:
;  APPLICANT: Demotz et al.
;  TITLE OF INVENTION: SYNTHETIC CHEMOKINES LABELED AT SELECTED POSITIONS
;  FILE REFERENCE: 29964/38772A
;  CURRENT APPLICATION NUMBER: US/10/668,733
;  CURRENT FILING DATE:  2003-09-23
;  PRIOR APPLICATION NUMBER: US 60/412,866
;  PRIOR FILING DATE: 2002-09-23
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
;   LENGTH: 72
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic peptide
US-10-668-733-18

  Query Match             73.4%;  Score 287;  DB 16;  Length 72;
  Best Local Similarity   76.1%;  Pred. No. 8.9e-26;
  Matches   51;  Conservative   10;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          2 ELRCQCIRTHSTPFHPKFIKELRVIESPPHCENSEIIVKLTNGNEVCLNPKEKWVQKVVQ 61
              |||||||:|:| |||||||||||||| ||| |:||||||::| |:||:||| |||:||:
Db          4 ELRCQCIKTYSKPFHPKFIKELRVIESGPHCANTEIIVKLSDGRELCLDPKENWVQRVVE 63

Qy         62 VFVKRAE 68
               |:||||
Db         64 KFLKRAE 70


RESULT 8
US-10-803-960-16
; Sequence 16, Application US/10803960
; Publication No. US20040156822A1
; GENERAL INFORMATION:
;  APPLICANT: White, John R.
;  APPLICANT:  Pelus, Louis
;  APPLICANT:  Li, Haodong
;  APPLICANT:  Kreider, Brent L.
;  TITLE OF INVENTION: Novel Chemokine for Mobilizing Stem Cells
;  FILE REFERENCE: PF497D2
;  CURRENT APPLICATION NUMBER: US/10/803,960
;  CURRENT FILING DATE:  2004-03-19
;  PRIOR APPLICATION NUMBER: 09/567,225
;  PRIOR FILING DATE: 2000-05-09
;  PRIOR APPLICATION NUMBER: US 09/225,501
;  PRIOR FILING DATE: 1999-01-06
;  PRIOR APPLICATION NUMBER: US 60/006,051
;  PRIOR FILING DATE: 1995-10-24
;  PRIOR APPLICATION NUMBER: US 08/740,033
;  PRIOR FILING DATE: 1996-10-23
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
;   LENGTH: 72
;   TYPE: PRT
;   ORGANISM: NAP-1/IL-8
US-10-803-960-16

  Query Match             73.4%;  Score 287;  DB 16;  Length 72;
  Best Local Similarity   76.1%;  Pred. No. 8.9e-26;
  Matches   51;  Conservative   10;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          2 ELRCQCIRTHSTPFHPKFIKELRVIESPPHCENSEIIVKLTNGNEVCLNPKEKWVQKVVQ 61
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Db          4 ELRCQCIKTYSKPFHPKFIKELRVIESGPHCANTEIIVKLSDGRELCLDPKENWVQRVVE 63

Qy         62 VFVKRAE 68
               |:||||
Db         64 KFLKRAE 70


RESULT 9
US-10-207-330-26
; Sequence 26, Application US/10207330
; Publication No. US20030018169A1
; GENERAL INFORMATION:
;  APPLICANT: Kochendoerfer, Gerd G
;  APPLICANT:  Hunter, Christie L
;  APPLICANT:  Kent, Stephen B.H.
;  APPLICANT:  Botti, Paolo
;  APPLICANT:  Gryphon Sciences
;  TITLE OF INVENTION: Lipid Matrix-Assisted Chemical Ligation and Synthesis
;  TITLE OF INVENTION:  of Membrane Polypeptides
;  FILE REFERENCE: grfn-028/02WO
;  CURRENT APPLICATION NUMBER: US/10/207,330
;  CURRENT FILING DATE:  2002-07-30
;  PRIOR APPLICATION NUMBER: US/09/384,302
;  PRIOR FILING DATE: 1999-08-26
;  PRIOR APPLICATION NUMBER: 09/144,964
;  PRIOR FILING DATE: 1998-08-31
;  PRIOR APPLICATION NUMBER: 09/263,971
;  PRIOR FILING DATE: 1999-03-05
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
;   LENGTH: 73
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:Synthetic
US-10-207-330-26

  Query Match             73.4%;  Score 287;  DB 14;  Length 73;
  Best Local Similarity   76.1%;  Pred. No. 9.1e-26;
  Matches   51;  Conservative   10;  Mismatches    6;  Indels    0;  Gaps    0;
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Qy          2 ELRCQCIRTHSTPFHPKFIKELRVIESPPHCENSEIIVKLTNGNEVCLNPKEKWVQKVVQ 61
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Qy         62 VFVKRAE 68
                |:||||
Db         64 KFLKRAE 70
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RESULT 10
US-10-104-755-79
; Sequence 79, Application US/10104755
; Publication No. US20030031645A1
; GENERAL INFORMATION:
; APPLICANT: Strieter, Robert M.
; Polverini, Peter J.
; Kunkel, Steven L.
; TITLE OF INVENTION: CXC Chemokines as Regulators of
; Angiogenesis
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: US
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/104,755
; FILING DATE: 21-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/213,383
; FILING DATE: 09-Dec-1998
; APPLICATION NUMBER: 08/468,819
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: UMIC:003/HYL
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7477
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 79:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 76 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 79:
US-10-104-755-79

Query Match 73.4%; Score 287; DB 14; Length 76;
Best Local Similarity 76.1%; Pred. No. 9.5e-26;
Matches 51; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

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Qy          2 ELRCQCIRTHSTPFHPKFIKELRVIESPPHCENSEIIVKLTNGNEVCLNPKEKWVQKVVQ 61
              |||||||:|:| |||||||||||||| ||| |:||||||::| |:||:||| |||:||:
Db          8 ELRCQCIKTYSKPFHPKFIKELRVIESGPHCANTEIIVKLSDGRELCLDPKENWVQRVVE 67

Qy         62 VFVKRAE 68
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Db         68 KFLKRAE 74
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RESULT 11
US-09-792-793A-19
; Sequence 19, Application US/09792793A
; Patent No. US20020168370A1
; GENERAL INFORMATION:
; APPLICANT: McDonald, John R.
; APPLICANT: Coggins, Philip
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AN
; TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS
; FILE REFERENCE: 25020-601D
; CURRENT APPLICATION NUMBER: US/09/792,793A
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 77
; TYPE: PRT
; ORGANISM: homo sapien
; FEATURE:
; OTHER INFORMATION: Human Chemokine Polypeptide: Interleukin-8 (IL-8)
US-09-792-793A-19

Query Match 73.4%; Score 287; DB 9; Length 77;
Best Local Similarity 76.1%; Pred. No. 9.6e-26;
Matches 51; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

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Qy          2 ELRCQCIRTHSTPFHPKFIKELRVIESPPHCENSEIIVKLTNGNEVCLNPKEKWVQKVVQ 61
              |||||||:|:| |||||||||||||| ||| |:||||||::| |:||:||| |||:||:
Db          9 ELRCQCIKTYSKPFHPKFIKELRVIESGPHCANTEIIVKLSDGRELCLDPKENWVQRVVE 68

Qy         62 VFVKRAE 68
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Db         69 KFLKRAE 75
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RESULT 12
US-09-811-162-4
; Sequence 4, Application US/09811162
; Publication No. US20030040109A1
; GENERAL INFORMATION:
; APPLICANT: Martins-Green, Manuela
; APPLICANT: Feugate, Jo Ellen
; APPLICANT: Li, QiJing
; TITLE OF INVENTION: Chemokines and Methods for Inducing the Differentiation of Fibrob
; TITLE OF INVENTION: Myofibroblasts
; FILE REFERENCE: 407E-000500US
; CURRENT APPLICATION NUMBER: US/09/811,162
; CURRENT FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Homosapiens
US-09-811-162-4

Query Match 73.4%; Score 287; DB 10; Length 77;
Best Local Similarity 76.1%; Pred. No. 9.6e-26;
Matches 51; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

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Qy          2 ELRCQCIRTHSTPFHPKFIKELRVIESPPHCENSEIIVKLTNGNEVCLNPKEKWVQKVVQ 61
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Qy         62 VFVKRAE 68
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Db         69 KFLKRAE 75
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RESULT 13
US-10-375-209A-19
; Sequence 19, Application US/10375209A
; Publication No. US20030215421A1

```
; GENERAL INFORMATION:
;  APPLICANT: McDonald, John R.
;  APPLICANT:  Coggins, Philip
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
;  TITLE OF INVENTION:  OTHER INFLAMMATORY CONDITIONS AND DISORDERS
;  FILE REFERENCE: 25020-601E
;  CURRENT APPLICATION NUMBER: US/10/375,209A
;  CURRENT FILING DATE:  2003-02-24
;  NUMBER OF SEQ ID NOS: 93
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
;   LENGTH: 77
;   TYPE: PRT
;   ORGANISM: homo sapien
;   FEATURE:
;   OTHER INFORMATION: Human Chemokine Polypeptide: Interleukin-8 (IL-8)
US-10-375-209A-19

  Query Match            73.4%;  Score 287;  DB 14;  Length 77;
  Best Local Similarity   76.1%;  Pred. No. 9.6e-26;
  Matches   51;  Conservative   10;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          2 ELRCQCIRTHSTPFHPKFIKELRVIESPPHCENSEIIVKLTNGNEVCLNPKEKWVQKVVQ 61
              |||||||:|:| |||||||||||||| ||| |:||||||::| |:||:||| |||:||:
Db          9 ELRCQCIKTYSKPFHPKFIKELRVIESGPHCANTEIIVKLSDGRELCLDPKENWVQRVVE 68

Qy         62 VFVKRAE 68
              |:||||
Db         69 KFLKRAE 75


RESULT 14
US-10-332-038A-22
; Sequence 22, Application US/10332038A
; Publication No. US20040077835A1
; GENERAL INFORMATION:
;  APPLICANT: Gryphon Therapeutics, Inc.
;  APPLICANT:  Offord, Robin
;  APPLICANT:  Gaertner, Hubert
;  APPLICANT:  Hartley, Oliver
;  TITLE OF INVENTION: Chemokine Receptor Modulators, Production and Use
;  FILE REFERENCE: 03504.271
;  CURRENT APPLICATION NUMBER: US/10/332,038A
;  CURRENT FILING DATE:  2003-05-06
;  PRIOR APPLICATION NUMBER: US 60/217,683
;  PRIOR FILING DATE: 2000-07-12
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22
;   LENGTH: 77
;   TYPE: PRT
;   ORGANISM: Homo Sapiens
US-10-332-038A-22

  Query Match            73.4%;  Score 287;  DB 15;  Length 77;
  Best Local Similarity   76.1%;  Pred. No. 9.6e-26;
  Matches   51;  Conservative   10;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          2 ELRCQCIRTHSTPFHPKFIKELRVIESPPHCENSEIIVKLTNGNEVCLNPKEKWVQKVVQ 61
              |||||||:|:| |||||||||||||| ||| |:||||||::| |:||:||| |||:||:
Db          9 ELRCQCIKTYSKPFHPKFIKELRVIESGPHCANTEIIVKLSDGRELCLDPKENWVQRVVE 68

Qy         62 VFVKRAE 68
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Db         69 KFLKRAE 75


RESULT 15
US-10-243-795-1
; Sequence 1, Application US/10243795
; Publication No. US20040197303A1
; GENERAL INFORMATION:
;  APPLICANT: CHEMOKINE THERAPEUTICS CORP.
;  TITLE OF INVENTION: DESIGN OF CHEMOKINE ANALOGS FOR THE TREATMENT OF HUMAN DISEASES
;  FILE REFERENCE: 59296.00003
;  CURRENT APPLICATION NUMBER: US/10/243,795
;  CURRENT FILING DATE:  2002-09-13
;  NUMBER OF SEQ ID NOS: 1640
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
;   LENGTH: 77
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
US-10-243-795-1

  Query Match            73.4%;  Score 287;  DB 17;  Length 77;
  Best Local Similarity   76.1%;  Pred. No. 9.6e-26;
  Matches   51;  Conservative   10;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          2 ELRCQCIRTHSTPFHPKFIKELRVIESPPHCENSEIIVKLTNGNEVCLNPKEKWVQKVVQ 61
              |||||||:|:| |||||||||||||| ||| |:||||||::| |:||:||| |||:||:
Db          9 ELRCQCIKTYSKPFHPKFIKELRVIESGPHCANTEIIVKLSDGRELCLDPKENWVQRVVE 68

Qy         62 VFVKRAE 68
              |:||||
Db         69 KFLKRAE 75


Search completed: December 13, 2004, 20:05:06
Job time : 148 secs
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OM protein - protein search, using sw model

Run on: December 13, 2004, 19:43:47 ; Search time 38 Seconds
(without alignments)
182.305 Million cell updates/sec

Title: US-10-087-273-1
Perfect score: 391
Sequence: 1 TELRCQCIRTHSTPFHPKFI.....EKWVQKVVQVFVKRAEKQDP 72

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	361	92.3	101	2	S42496	interleukin-8 prec
2	335	85.7	103	2	A53096	interleukin-8 prec
3	330	84.4	101	2	I46871	interleukin-8 - ra
4	318	81.3	95	2	JN0841	interleukin-8 - do
5	287	73.4	99	2	A37034	interleukin-8 prec
6	280	71.6	101	2	I48148	Neutrophil attract
7	193	49.4	103	2	I50417	RSV-induced protei
8	193	49.4	103	2	A26736	transformation-ind
9	165.5	42.3	117	2	B44253	alveolar macrophag
10	161.5	41.3	96	2	A32954	gro-alpha precurso
11	161.5	41.3	101	2	B28414	growth-regulated p
12	154.5	39.5	96	2	JN0572	neutrophil chemo-a
13	148.5	38.0	75	2	B54188	granulocyte chemot
14	145.5	37.2	107	2	A28414	melanoma growth-st
15	144.5	37.0	107	2	JH0281	macrophage inflamm
16	144.5	37.0	114	2	A55010	neutrophil-activat
17	142.5	36.4	107	2	B38290	GRO-gamma precurso
18	138.5	35.4	75	2	A54188	granulocyte chemot
19	138.5	35.4	128	1	TGHU	beta-thromboglobul
20	137.5	35.2	132	2	A57325	C-X-C chemokine LI
21	136.5	34.9	100	2	I55614	macrophage inflamm
22	136.5	34.9	100	2	S21467	macrophage inflamm
23	135.5	34.7	100	2	S46198	cytokine-induced n
24	130.5	33.4	100	2	JH0200	macrophage inflamm
25	127.5	32.6	119	2	S42881	platelet basic pro
26	125	32.0	126	2	A35766	platelet factor 4,
27	124	31.7	125	2	JN0470	interferon gamma-i
28	123.5	31.6	90	2	S69133	platelet factor 4
29	121	30.9	105	2	A26774	platelet factor 4
30	118	30.2	53	2	I64831	gene KC protein -
31	115.5	29.5	101	1	PFHU4	platelet factor 4
32	114.5	29.3	104	1	PFHU4A	platelet factor 4
33	112.5	28.8	98	1	TGHUGI	interferon gamma-i
34	110	28.1	53	2	I51886	macrophage inflamm
35	108.5	27.7	98	2	I59277	Mob-1 - rat
36	103.5	26.5	98	2	A45492	IP-10 precursor -
37	101.5	26.0	113	2	JC7800	neutrophil activat
38	91.5	23.4	88	1	PFBO4	platelet factor 4
39	87	22.3	89	2	I53416	interleukin-8 homo
40	87	22.3	89	2	A53497	pre-B-cell growth-
41	87	22.3	93	2	I81182	cytokine - mouse
42	86	22.0	93	2	G01540	cytokine SDF-1-bet
43	81	20.7	99	1	A39296	monocyte chemoattr
44	81	20.7	99	2	JC2336	monocyte chemoattr
45	80.5	20.6	36	2	S17507	cytokine - rabbit

ALIGNMENTS

RESULT 1
S42496
interleukin-8 precursor [similarity] - sheep
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: S42496; I46997
R;Legastelois, I.; Greenland, T.; Arnaud, P.; Mornex, J.F.; Cordier, G.
submitted to the EMBL Data Library, March 1994
A;Description: Nucleotide sequence of ovine interleukin 8 cDNA using polymerase chain r
A;Reference number: S42496
A;Accession: S42496
A;Molecule type: mRNA
A;Residues: 1-101 <LEG>
A;Cross-references: UNIPROT:P36925; EMBL:X78306; NID:g463253; PIDN:CAA55115.1; PID:g463
R;Seow, H.F.; Yoshimura, T.; Wood, P.R.; Colditz, I.G.
Immunol. Cell Biol. 72, 398-405, 1994
A;Title: Cloning, sequencing, expression and inflammatory activity in skin of ovine int
A;Reference number: I46997; MUID:95137691; PMID:7835984
A;Accession: I46997
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-101 <SEO>
A;Cross-references: GB:S74436; NID:g786590; PIDN:AAB33241.1; PID:g786591
C;Genetics:
A;Gene: IL-8
C;Superfamily: beta-thromboglobulin
C;Keywords: chemotaxis; cytokine; inflammation
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-101/Product: interleukin-8 #status predicted <MAT>

Query Match 92.3%; Score 361; DB 2; Length 101;
Best Local Similarity 91.7%; Pred. No. 1.5e-33;
Matches 66; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

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Qy          1 TELRCQCIRTHSTPFHPKFIKELRVIESPPHCENSEIIVKLTNGNEVCLNPKEKWVQKVV 60
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Db         30 TELRCQCIKTHSTPFHPKFIKELRVIESGPHCENSEIIVKLTNGKEVCLDPKEKWVQKVV 89

Qy         61 QVFVKRAEKQDP 72
              | |:||||||||
Db         90 QAFLKRAEKQDP 101
```

RESULT 2
A53096
interleukin-8 precursor - pig
N;Alternate names: alveolar macrophage chemotactic factor-I (AMCF-I)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 02-Jun-1995 #sequence_revision 02-Jun-1995 #text_change 09-Jul-2004
C;Accession: A53096; A44253
R;Lin, G.; Pearson, A.E.; Scamurra, R.W.; Zhou, Y.; Baarsch, M.J.; Weiss, D.J.; Murtaug
J. Biol. Chem. 269, 77-85, 1994

```
A;Title: Regulation of interleukin-8 expression in porcine alveolar macrophages by bacte
A;Reference number: A53096; MUID:94103307; PMID:8276881
A;Accession: A53096
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-103 <LIN>
A;Cross-references: UNIPROT:P26894; GB:M86923; NID:g164520; PIDN:AAA16616.1; PID:g164521
R;Goodman, R.B.; Foster, D.C.; Mathewes, S.L.; Osborn, S.G.; Kuijper, J.L.; Forstrom, J.
Biochemistry 31, 10483-10490, 1992
A;Title: Molecular cloning of porcine alveolar macrophage-derived neutrophil chemotactic
A;Reference number: A44253; MUID:93041741; PMID:1420165
A;Accession: A44253
A;Status: preliminary
A;Molecule type: mRNA; protein
A;Residues: 1-22,'D',24-103 <GOO>
A;Cross-references: GB:M99367; NID:g1235611
A;Experimental source: alveolar macrophage
A;Note: sequence extracted from NCBI backbone (NCBIN:117415, NCBIP:117416)
A;Note: the sequence in GenBank entry PIGAMCFI, release 117.0, has been corrected to cor
C;Superfamily: beta-thromboglobulin
C;Keywords: chemotaxis; cytokine; inflammation
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-103/Product: interleukin-8 #status predicted <MAT>

  Query Match             85.7%;  Score 335;  DB 2;  Length 103;
  Best Local Similarity   88.4%;  Pred. No. 1.3e-30;
  Matches   61;  Conservative    3;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          2 ELRCQCIRTHSTPFHPKFIKELRVIESPPHCENSEIIVKLTNGNEVCLNPKEKWVQKVVQ 61
              ||||||| |||||||||||||||||||| |||||||||| || ||||:|||||||||||
Db         31 ELRCQCINTHSTPFHPKFIKELRVIESGPHCENSEIIVKLVNGKEVCLDPKEKWVQKVVQ 90

Qy         62 VFVKRAEKQ 70
              :|:|| |||
Db         91 IFLKRTEKQ 99


RESULT 3
I46871
interleukin-8 - rabbit
N;Alternate names: neutrophil attractant/activation protein-1
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 09-Jul-2004
C;Accession: I46871; S13052
R;Yoshimura, T.; Yuhki, N.
J. Immunol. 146, 3483-3488, 1991
A;Title: Neutrophil attractant/activation protein-1 and monocyte chemoattractant protein
A;Reference number: I46857; MUID:91225489; PMID:2026877
A;Accession: I46871
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-101 <YOS>
A;Cross-references: UNIPROT:P19874; GB:M57439; NID:g165552; PIDN:AAA31422.1; PID:g165553
R;Beaubien, B.C.; Collins, P.D.; Jose, P.J.; Totty, N.F.; Hsuan, J.; Waterfield, M.D.; W
Biochem. J. 271, 797-801, 1990
A;Title: A novel neutrophil chemoattractant generated during an inflammatory reaction in
 interleukin 8.
A;Reference number: S13052; MUID:91058518; PMID:2244880
A;Accession: S13052
A;Molecule type: protein
A;Residues: 23-33,'X',35,'X',37-46,'X',48-49,'I',51-53 <BEA>
C;Superfamily: beta-thromboglobulin
C;Keywords: cytokine

  Query Match             84.4%;  Score 330;  DB 2;  Length 101;
  Best Local Similarity   83.1%;  Pred. No. 4.5e-30;
  Matches   59;  Conservative    8;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 TELRCQCIRTHSTPFHPKFIKELRVIESPPHCENSEIIVKLTNGNEVCLNPKEKWVQKVV 60
              ||||||||:||||||||||||||||||| ||| |||||||| :| |:||:|||||||||||
Db         30 TELRCQCIKTHSTPFHPKFIKELRVIESGPHCANSEIIVKLVDGRELCLDPKEKWVQKVV 89

Qy         61 QVFVKRAEKQD 71
                  |:|:||||:|:
Db         90 QIFLKRAEQQE 100


RESULT 4
JN0841
interleukin-8 - dog
C;Species: Canis lupus familiaris (dog)
C;Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 12-Apr-1995
C;Accession: JN0841
R;Ishikawa, J.; Suzuki, S.; Hotta, K.; Hirota, Y.; Mizuno, S.; Suzuki, K.
Gene 131, 305-306, 1993
A;Title: Cloning of a canine gene homologous to the human interleukin-8-encoding gene.
A;Reference number: JN0841; MUID:94010328; PMID:7916715
A;Accession: JN0841
A;Molecule type: DNA
A;Residues: 1-95 <ISH>
C;Comment: This protein is a polymorphonuclear leukocyles chemotactic factor and is invo
C;Genetics:
A;Introns: 22/1; 67/2
C;Superfamily: beta-thromboglobulin

  Query Match             81.3%;  Score 318;  DB 2;  Length 95;
  Best Local Similarity   84.8%;  Pred. No. 9.5e-29;
  Matches   56;  Conservative    8;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TELRCQCIRTHSTPFHPKFIKELRVIESPPHCENSEIIVKLTNGNEVCLNPKEKWVQKVV 60
              :|||||||:|||||||||:|||||||:| |||||||||||| ||||||:||||||||||
Db         30 SELRCQCIKTHSTPFHPKYIKELRVIDSGPHCENSEIIVKLFNGNEVCLDPKEKWVQKVV 89

Qy         61 QVFVKR 66
              |:|:|:
Db         90 QIFLKK 95


RESULT 5
A37034
interleukin-8 precursor - human
N;Alternate names: beta-thromboglobulin-like protein; fibroblast-derived neutrophil-acti
te-derived neutrophil chemotactic factor; monocyte-derived neutrophil-activating factor
C;Species: Homo sapiens (man)
C;Date: 08-Dec-1992 #sequence_revision 08-Dec-1992 #text_change 09-Jul-2004
C;Accession: A37034; JL0041; A32791; S37634; PL0107; A28598; A27488; A39960; A60401; A6C
R;Mukaida, N.; Shiroo, M.; Matsushima, K.
J. Immunol. 143, 1366-1371, 1989
A;Title: Genomic structure of the human monocyte-derived neutrophil chemotactic factor I
A;Reference number: A37034; MUID:89309826; PMID:2663993
A;Accession: A37034
A;Molecule type: DNA
A;Residues: 1-99 <MUK>
A;Cross-references: UNIPROT:P10145; GB:M28130; NID:g186367; PIDN:AAA59158.1; PID:g186368
A;Note: the authors failed to translate the last thirty-six nucleotides of the second ex
R;Matsushima, K.; Morishita, K.; Yoshimura, T.; Lavu, S.; Kobayashi, Y.; Lew, W.; Appell
J. Exp. Med. 167, 1883-1893, 1988
A;Title: Molecular cloning of a human monocyte-derived neutrophil chemotactic factor (MI
A;Reference number: JL0041; MUID:88258376; PMID:3260265
A;Accession: JL0041
A;Molecule type: mRNA
A;Residues: 1-99 <MA1>
A;Cross-references: EMBL:Y00787; NID:g34518; PIDN:CAA68742.1; PID:g34519
A;Note: the sequence shows similarity to several platelet-derived factors, a v-src-induc
R;Kowalski, J.; Denhardt, D.T.
Mol. Cell. Biol. 9, 1946-1957, 1989
A;Title: Regulation of the mRNA for monocyte-derived neutrophil-activating peptide in di
A;Reference number: A32791; MUID:89313739; PMID:2664463
A;Accession: A32791
A;Molecule type: mRNA
A;Residues: 1-99 <KOW>
A;Cross-references: GB:M26383; NID:g188627; PIDN:AAA36323.1; PID:g188628
R;King, C.H.; Gordon, G.S.; Konieczkowski, M.; Sedor, J.R.
submitted to the EMBL Data Library, February 1992
A;Reference number: S37634
A;Accession: S37634
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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-97 <KIN>
A;Cross-references: EMBL:Z11686; NID:g33958; PIDN:CAA77745.1; PID:g33959
R;Suzuki, K.; Miyasaka, H.; Ota, H.; Yamakawa, Y.; Tagawa, M.; Kuramoto, A.; Mizuno, S.
J. Exp. Med. 169, 1895-1901, 1989
A;Title: Purification and partial primary sequence of a chemotactic protein for polymorp
A;Reference number: PL0107; MUID:89279141; PMID:2659722
A;Accession: PL0107
A;Molecule type: protein
A;Residues: 23-32,'XR',35,'X',37-52,'L',54 <SUZ>
A;Experimental source: lung giant cell carcinoma LU65C
R;Gregory, H.; Young, J.; Schroeder, J.M.; Mrowietz, U.; Christophers, E.
Biochem. Biophys. Res. Commun. 151, 883-890, 1988
A;Title: Structure determination of a human lymphocyte derived neutrophil activating pep
A;Reference number: A28598; MUID:88162914; PMID:3279957
A;Accession: A28598
A;Molecule type: protein
A;Residues: 28-99 <GRE>
R;Walz, A.; Peveri, P.; Aschauer, H.; Baggiolini, M.
Biochem. Biophys. Res. Commun. 149, 755-761, 1987
A;Title: Purification and amino acid sequencing of NAF, a novel neutrophil-activating fa
A;Reference number: A27488; MUID:88106502; PMID:3322281
A;Accession: A27488
A;Molecule type: protein
A;Residues: 28-59 <WAL>
R;Yoshimura, T.; Matsushima, K.; Tanaka, S.; Robinson, E.A.; Appella, E.; Oppenheim, J.J
Proc. Natl. Acad. Sci. U.S.A. 84, 9233-9237, 1987
A;Title: Purification of a human monocyte-derived neutrophil chemotactic factor that has
A;Reference number: A39960; MUID:88097462; PMID:3480540
A;Accession: A39960
A;Molecule type: protein
A;Residues: 28-69 <YOS>
R;Schroeder, J.M.; Sticherling, M.; Henneicke, H.H.; Preissner, W.C.; Christophers, E.
J. Immunol. 144, 2223-2232, 1990
A;Title: IL-1alpha or tumor necrosis factor-alpha stimulate release of three NAP-1/IL-8-
A;Reference number: A60401; MUID:90187866; PMID:2179408
A;Accession: A60401
A;Molecule type: protein
A;Residues: 23-32 <SCH>
A;Experimental source: dermal fibroblasts
A;Note: a minor component of this material (15%) includes an additional two amino acids
R;Van Damme, J.; Decock, B.; Conings, R.; Lenaerts, J.P.; Opdenakker, G.; Billiau, A.
Eur. J. Immunol. 19, 1189-1194, 1989
A;Title: The chemotactic activity for granulocytes produced by virally infected fibrobla
A;Reference number: A60591; MUID:89338542; PMID:2668011
A;Accession: A60591
A;Molecule type: protein
A;Residues: 23-33,'X',35,'X',37-42 <VAN>
R;Nakagawa, H.; Hatakeyama, S.; Ikesue, A.; Miyai, H.
FEBS Lett. 282, 412-414, 1991
A;Title: Generation of interleukin-8 by plasmin from AVLPR-interleukin-8, the human fibr
A;Reference number: S15827; MUID:91243843; PMID:1828038
A;Accession: S15827
A;Molecule type: protein
A;Residues: 23-33,'X',35,'X',37-47 <FEB>
R;van Damme, J.; van Beeumen, J.; Conings, R.; Decock, B.; Billiau, A.
Eur. J. Biochem. 181, 337-344, 1989
A;Title: Purification of granulocyte chemotactic peptide/interleukin-8 reveals N-termina
A;Reference number: S04216; MUID:89231715; PMID:2523801
A;Accession: S04216
A;Molecule type: protein
A;Residues: 21-67 <VA2>
R;Yoshimura, T.; Robinson, E.A.; Appella, E.; Matsushima, K.; Showalter, S.D.; Skeel, A.
Mol. Immunol. 26, 87-93, 1989
A;Title: Three forms of monocyte-derived neutrophil chemotactic factor (MDNCF) distingui
A;Reference number: A60567; MUID:89181632; PMID:2648135
A;Accession: A60567
A;Molecule type: protein
A;Residues: 21-33,'X',35,'X',37-47 <YO2>
A;Note: the forms starting from positions 21, 23, and 28 represented 8%, 47%, and 45%, r
R;Van Damme, J.; Van Beeumen, J.; Opdenakker, G.; Billiau, A.
J. Exp. Med. 167, 1364-1376, 1988

A;Title: A novel, NH-2-terminal sequence-characterized human monokine possessing neutro
A;Reference number: A60847; MUID:88187604; PMID:3258625
A;Accession: A60847
A;Molecule type: protein
A;Residues: 28-47 <VA3>
R;Car, B.D.; Baggiolini, M.; Walz, A.
Biochem. J. 275, 581-584, 1991
A;Title: Formation of neutrophil-activating peptide 2 from platelet-derived connective-
A;Reference number: S15417; MUID:91248085; PMID:2039437
A;Accession: S15417
A;Status: preliminary
A;Molecule type: protein
A;Residues: 28-99 <CAR>
R;Golds, E.E.; Mason, P.; Nyirkos, P.
Biochem. J. 259, 585-588, 1989
A;Title: Inflammatory cytokines induce synthesis and secretion of gro protein and a neu
A;Reference number: S03975; MUID:89246368; PMID:2655583
A;Accession: S03975
A;Molecule type: protein
A;Residues: 23-46 <GOL>
R;Hotta, K.; Hayashi, K.; Ishikawa, J.; Tagawa, M.; Hashimoto, K.; Mizumo, S.; Suzuki, I
Immunol. Lett. 24, 165-170, 1990
A;Title: Coding region structure of interleukin-8 gene of human lung giant cell carcino
A;Reference number: I54560; MUID:90346419; PMID:2200751
A;Accession: I54560
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-99 <RES>
A;Cross-references: GB:D14283; NID:g219915; PIDN:BAA03245.1; PID:g219916
R;Schmid, J.; Weissmann, C.
J. Immunol. 139, 250-256, 1987
A;Title: Induction of mRNA for a serine protease and a beta-thromboglobulin-like protei
A;Reference number: I55992; MUID:87224164; PMID:2953813
A;Accession: I55992
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-99 <RE2>
A;Cross-references: GB:M17017; NID:g179579; PIDN:AAA35611.1; PID:g179580
R;Kusner, D.J.; Luebbers, E.L.; Nowinski, R.J.; Konieczkowski, M.; King, C.H.; Sedor, J
Kidney Int. 39, 1240-1248, 1991
A;Title: Cytokine- and LPS-induced synthesis of interleukin-8 from human mesangial cell
A;Reference number: I37902; MUID:91374977; PMID:1895676
A;Accession: I37902
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-97 <RE3>
A;Cross-references: EMBL:Z11686; NID:g33958; PIDN:CAA77745.1; PID:g33959
R;Alouani, S.; Gaertner, H.F.; Mermod, J.J.; Power, C.A.; Bacon, K.B.; Wells, T.N.C.; P
Eur. J. Biochem. 227, 328-334, 1995
A;Title: A fluorescent interleukin-8 receptor probe produced by targetted labelling at
A;Reference number: S67519; MUID:95154308; PMID:7851404
A;Accession: S67519
A;Molecule type: mRNA
A;Residues: 1-99 <ALO>
C;Comment: This secretory protein is chemotactic for polymorphonuclear leukocytes.
C;Comment: This protein is variably processed at the amino end. The major form differs
C;Genetics:
A;Gene: GDB:IL8
A;Cross-references: GDB:120099; OMIM:146930
A;Map position: 4q13-4q21
A;Introns: 22/1; 67/2; 95/2
C;Superfamily: beta-thromboglobulin
C;Keywords: chemotaxis; cytokine; inflammation
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-99/Product: interleukin-8, minor form #status experimental <MATA>
F;23-99/Product: interleukin-8, major fibroblast-derived form #status experimental <MATI
F;28-99/Product: interleukin-8, major lymphocyte/monocyte-derived form #status experime

Query Match 73.4%; Score 287; DB 2; Length 99;
Best Local Similarity 76.1%; Pred. No. 3e-25;
Matches 51; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

Qy 2 ELRCQCIRTHSTPFHPKFIKELRVIESPPHCENSEIIVKLTNGNEVCLNPKEKWVQKVVQ 61

```
Db          31 ELRCQCIKTYSKPFHPKFIKELRVIESGPHCANTEIIVKLSDGRELCLDPKENWVQRVVE 90

Qy          62 VFVKRAE 68
               |:||||
Db          91 KFLKRAE 97


RESULT 6
I48148
Neutrophil attractant protein-1 - guinea pig
C;Species: Cavia porcellus (guinea pig)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I48148
R;Yoshimura, T.; Johnson, D.G.
J. Immunol. 151, 6225-6236, 1993
A;Title: cDNA cloning and expression of guinea pig neutrophil attractant protein-1 (NAP-
A;Reference number: I48148; MUID:94065176; PMID:7504015
A;Accession: I48148
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-101 <RES>
A;Cross-references: UNIPROT:P49113; GB:L04986; NID:g459764; PIDN:AAA37049.1; PID:g459765
C;Genetics:
A;Gene: NAP-1
C;Superfamily: beta-thromboglobulin

  Query Match             71.6%;  Score 280;  DB 2;  Length 101;
  Best Local Similarity   69.0%;  Pred. No. 1.9e-24;
  Matches   49;  Conservative   12;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 TELRCQCIRTHSTPFHPKFIKELRVIESPPHCENSEIIVKLTNGNEVCLNPKEKWVQKVV 60
              :|||||||: |:|||||||||||:|||| | | |||||||||::  ::||:||:|||| ||
Db         30 SELRCQCIKIHTTPFHPKFIKELKVIESGPRCANSEIIVKLSDNRQLCLDPKKKWVQDVV 89

Qy         61 QVFVKRAEKQD 71
              :|:|| | ||
Db         90 SMFLKRTESQD 100


RESULT 7
I50417
RSV-induced protein - chicken
C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: I50417
R;Bedard, P.
Proc. Natl. Acad. Sci. U.S.A. 84, 6715-6719, 1987
A;Title: Constitutive expression of a gene encoding a polypeptide homologous to biologic

A;Reference number: I50417; MUID:88016162; PMID:2821543
A;Accession: I50417
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-103 <BED>
A;Cross-references: UNIPROT:P08317; GB:J02975; NID:g212643; PIDN:AAA49059.1; PID:g212644
C;Superfamily: beta-thromboglobulin

  Query Match             49.4%;  Score 193;  DB 2;  Length 103;
  Best Local Similarity   50.7%;  Pred. No. 1.2e-14;
  Matches   34;  Conservative   13;  Mismatches   20;  Indels    0;  Gaps    0;

Qy          2 ELRCQCIRTHSTPFHPKFIKELRVIESPPHCENSEIIVKLTNGNEVCLNPKEKWVQKVVQ 61
              |||||||  |||    |||  |:::::  | |||:| |||  | :| ||||:|   ||| :|:
Db         30 ELRCQCISTHSKFIHPKSIQDVKLTPSGPHCKNVEIIATLKDGREVCLDPTAPWVQLIVK 89

Qy         62 VFVKRAE 68
                : :|:
Db         90 ALMAKAQ 96


RESULT 8
A26736
transformation-induced protein precursor (clone 9E3) - chicken
C;Species: Gallus gallus (chicken)
C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 09-Jul-2004
C;Accession: A26736
R;Sugano, S.; Stoeckle, M.Y.; Hanafusa, H.
Cell 49, 321-328, 1987
A;Title: Transformation by Rous sarcoma virus induces a novel gene with homology to a mi
A;Reference number: A26736; MUID:87187628; PMID:3032449
A;Accession: A26736
A;Molecule type: mRNA
A;Residues: 1-103 <SUG>
A;Cross-references: UNIPROT:P08317; GB:M16199; NID:g211735; PIDN:AAA48758.1; PID:g211736
C;Superfamily: beta-thromboglobulin
C;Keywords: growth factor
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-103/Product: transformation-induced protein #status predicted <MAT>

  Query Match             49.4%;  Score 193;  DB 2;  Length 103;
  Best Local Similarity   50.7%;  Pred. No. 1.2e-14;
  Matches   34;  Conservative   13;  Mismatches   20;  Indels    0;  Gaps    0;

Qy          2 ELRCQCIRTHSTPFHPKFIKELRVIESPPHCENSEIIVKLTNGNEVCLNPKEKWVQKVVQ 61
              |||||||  |||    |||  |:::::  | |||:| |||  | :| ||||:|   ||| :|:
Db         30 ELRCQCISTHSKFIHPKSIQDVKLTPSGPHCKNVEIIATLKDGREVCLDPTAPWVQLIVK 89

Qy         62 VFVKRAE 68
                : :|:
Db         90 ALMAKAQ 96


RESULT 9
B44253
alveolar macrophage chemotactic factor-II (AMCF-II) intercrine-alpha protein - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: B44253
R;Goodman, R.B.; Foster, D.C.; Mathewes, S.L.; Osborn, S.G.; Kuijper, J.L.; Forstrom, J
Biochemistry 31, 10483-10490, 1992
A;Title: Molecular cloning of porcine alveolar macrophage-derived neutrophil chemotactic
A;Reference number: A44253; MUID:93041741; PMID:1420165
A;Accession: B44253
A;Status: preliminary
A;Molecule type: mRNA; protein
A;Residues: 1-117 <GOO>
A;Cross-references: UNIPROT:P22952; GB:M99368; NID:g164325; PIDN:AAA30991.1; PID:g164326
A;Experimental source: alveolar macrophage
A;Note: sequence extracted from NCBI backbone (NCBIN:117417, NCBIP:117418)
C;Superfamily: beta-thromboglobulin

  Query Match             42.3%;  Score 165.5;  DB 2;  Length 117;
  Best Local Similarity   45.1%;  Pred. No. 1.7e-11;
  Matches   32;  Conservative   14;  Mismatches   22;  Indels    3;  Gaps    2;

Qy          2 ELRCQCIRTHSTP-FHPKFIKELRVIESPPHCENSEIIVKLTNGNEVCLNPKEKWVQKVV 60
              |||| |: |  ||  ||| | :|:|| : | |  :|:|  | || ||||:||   ::|:|
Db         49 ELRCMCLTT--TPGIHPKMISDLQVIPAGPQCSKAEVIATLKNGKEVCLDPKAPLIKKIV 106

Qy         61 QVFVKRAEKQD 71
              |  :   :|::
Db        107 QKMLDSGKKKN 117


RESULT 10
A32954
gro-alpha precursor - mouse
N;Alternate names: gro protein; growth regulated protein; melanoma growth-stimulating ac
C;Species: Mus musculus (house mouse)
C;Date: 20-Oct-1989 #sequence_revision 20-Oct-1989 #text_change 09-Jul-2004
C;Accession: A32954; JH0081
R;Oquendo, P.; Alberta, J.; Wen, D.; Graycar, J.L.; Derynck, R.; Stiles, C.D.
J. Biol. Chem. 264, 4133-4137, 1989
A;Title: The platelet-derived growth factor-inducible KC gene encodes a secretory protei
A;Reference number: A32954; MUID:89139485; PMID:2917992
```

A;Accession: A32954
A;Molecule type: mRNA
A;Residues: 1-96 <OQU>
A;Cross-references: UNIPROT:P12850; GB:J04596; NID:g201042; PIDN:AAA40131.1; PID:g201043
R;Ryseck, R.P.; MacDonald-Bravo, H.; Mattei, M.G.; Bravo, R.
Exp. Cell Res. 180, 266-275, 1989
A;Title: Cloning and sequence of a secretory protein induced by growth factors in mouse
A;Reference number: JH0081; MUID:89078502; PMID:2909392
A;Accession: JH0081
A;Molecule type: mRNA
A;Residues: 1-96 <RYS>
C;Comment: This protein is basic and lacks threonine, phenylalanine, and tyrosine.
C;Genetics:
A;Map position: 5
C;Superfamily: beta-thromboglobulin
C;Keywords: extracellular protein
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-96/Product: gro-alpha #status predicted <MAT>

Query Match 41.3%; Score 161.5; DB 2; Length 96;
Best Local Similarity 47.1%; Pred. No. 3.8e-11;
Matches 32; Conservative 11; Mismatches 24; Indels 1; Gaps 1;

Qy 2 ELRCQCIRTHSTPFHPKFIKELRVIESPPHCENSEIIVKLTNGNEVCLNPKEKWVQKVVQ 61
Db 30 ELRCQCLQT-MAGIHLKNIQSLKVLPSGPHCTQTEVIATLKNGREACLDPEAPLVQKIVQ 88

Qy 62 VFVKRAEK 69
Db 89 KMLKGVPK 96

RESULT 11
B28414
growth-regulated protein precursor - Chinese hamster
C;Species: Cricetulus griseus (Chinese hamster)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C;Accession: B28414
R;Anisowicz, A.; Bardwell, L.; Sager, R.
Proc. Natl. Acad. Sci. U.S.A. 84, 7188-7192, 1987
A;Title: Constitutive overexpression of a growth-regulated gene in transformed Chinese h
A;Reference number: A94184; MUID:88041072; PMID:2890161
A;Accession: B28414
A;Molecule type: mRNA
A;Residues: 1-101 <ANI>
A;Cross-references: UNIPROT:P09340; GB:J03560; NID:g191088; PIDN:AAA36985.1; PID:g304509
A;Note: the authors translated the codon CAG for residue 52 as Glu
C;Superfamily: beta-thromboglobulin
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-101/Product: growth-regulated protein #status predicted <MAT>

Query Match 41.3%; Score 161.5; DB 2; Length 101;
Best Local Similarity 50.0%; Pred. No. 4.1e-11;
Matches 32; Conservative 9; Mismatches 22; Indels 1; Gaps 1;

Qy 2 ELRCQCIRTHSTPFHPKFIKELRVIESPPHCENSEIIVKLTNGNEVCLNPKEKWVQKVVQ 61
Db 34 ELRCQCLQT-MTGVHLKNIQSLKVTPPGPHCTQTEVIATLKNGQEACLNPEAPMVQKIVQ 92

Qy 62 VFVK 65
Db 93 KMLK 96

RESULT 12
JN0572
neutrophil chemo-attractant Gro protein precursor - rat
N;Alternate names: CINC; cytokine-induced neutrophil chemoattractant; interleukin-8-like
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: JN0572; JQ1519; A34481; A48988; B48988; S51214
R;Konishi, K.; Takata, Y.; Yamamoto, M.; Yomogida, K.; Watanabe, K.; Tsurufuji, S.; Fuji
Gene 126, 285-286, 1993
A;Title: Structure of the gene encoding rat neutrophil chemo-attractant Gro.
A;Reference number: JN0572; MUID:93246259; PMID:8482545
A;Accession: JN0572
A;Molecule type: DNA
A;Residues: 1-96 <KON>
A;Cross-references: UNIPROT:P14095; DDBJ:D11445; NID:g391854; PIDN:BAA02009.1; PID:g220
R;Huang, S.; Paulauskis, J.D.; Kobzik, L.
Biochem. Biophys. Res. Commun. 184, 922-929, 1992
A;Title: Rat KC cDNA cloning and mRNA expression in lung macrophages and fibroblasts.
A;Reference number: JQ1519; MUID:92246987; PMID:1374243
A;Accession: JQ1519
A;Molecule type: mRNA
A;Residues: 1-32,'S',34-96 <HUA>
A;Cross-references: GB:M86536
A;Experimental source: alveolar macrophage
A;Note: the authors translated the codon AGT for residue 33 as Cys, AAC for residue 46
R;Watanabe, K.; Konishi, K.; Fujioka, M.; Kinoshita, S.; Nakagawa, H.
J. Biol. Chem. 264, 19559-19563, 1989
A;Title: The neutrophil chemoattractant produced by the rat kidney epithelioid cell lin
A;Reference number: A34481; MUID:90062049; PMID:2684956
A;Accession: A34481
A;Molecule type: protein
A;Residues: 25-96 <WAT>
R;Nakagawa, H.; Ikesue, A.; Hatakeyama, S.; Kato, H.; Gotoda, T.; Komorita, N.; Watanab
Biochem. Pharmacol. 45, 1425-1430, 1993
A;Title: Production of an interleukin-8-like chemokine by cytokine-stimulated rat NRK-4
A;Reference number: A48988; MUID:93228656; PMID:8471066
A;Accession: A48988
A;Status: preliminary
A;Molecule type: protein
A;Residues: 25-57 <NAK>
A;Experimental source: kidney, NRK-49F fibroblasts
A;Note: sequence extracted from NCBI backbone (NCBIP:129132)
A;Accession: B48988
A;Status: preliminary
A;Molecule type: protein
A;Residues: 25-57 <NA2>
A;Experimental source: kidney, NRK-49F fibroblasts
A;Note: sequence extracted from NCBI backbone (NCBIP:129131)
R;Hanzawa, H.; Haruyama, H.; Watanabe, K.; Tsurufuji, S.
FEBS Lett. 354, 207-212, 1994
A;Title: The three dimensional structure of rat cytokine CINC/Gro in solution by homonu
A;Reference number: S51214; MUID:95046335; PMID:7957925
A;Contents: annotation; conformation by (1)H-NMR, residues 25-96
A;Accession: S51214
A;Molecule type: protein
A;Residues: 25-96 <HAN>
C;Comment: This protein has chemotactic activity for neutrophils and has melanoma growt
C;Genetics:
A;Gene: gro; KC
A;Introns: 24/1; 65/2; 92/2
C;Superfamily: beta-thromboglobulin
C;Keywords: cytokine; disulfide bond
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-96/Product: neutrophil chemo-attractant Gro protein #status experimental <CYT>

Query Match 39.5%; Score 154.5; DB 2; Length 96;
Best Local Similarity 45.6%; Pred. No. 2.3e-10;
Matches 31; Conservative 11; Mismatches 25; Indels 1; Gaps 1;

Qy 2 ELRCQCIRTHSTPFHPKFIKELRVIESPPHCENSEIIVKLTNGNEVCLNPKEKWVQKVVQ 61
Db 30 ELRCQCLQT-VAGIHFKNIQSLKVMPPGPHCTQTEVIATLKNGREACLDPEAPMVQKIVQ 88

Qy 62 VFVKRAEK 69
Db 89 KMLKGVPK 96

RESULT 13
B54188
granulocyte chemotactic protein, GCP-2 - bovine
C;Species: Bos primigenius taurus (cattle)

```
C;Date: 13-Sep-1994 #sequence_revision 18-Nov-1994 #text_change 12-Apr-1995
C;Accession: B54188
R;Proost, P.; Wuyts, A.; Conings, R.; Lenaerts, J.P.; Billiau, A.; Opdenakker, G.; Van D
Biochemistry 32, 10170-10177, 1993
A;Title: Human and bovine granulocyte chemotactic protein-2: complete amino acid sequenc
A;Reference number: A54188; MUID:94001982; PMID:8399143
A;Accession: B54188
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-75 <PRO>
A;Experimental source: MDBK cells
A;Note: sequence extracted from NCBI backbone (NCBIP:137967)
C;Superfamily: beta-thromboglobulin

  Query Match             38.0%;  Score 148.5;  DB 2;  Length 75;
  Best Local Similarity   47.5%;  Pred. No. 8.5e-10;
  Matches   29;  Conservative   11;  Mismatches   18;  Indels    3;  Gaps    2;

Qy          2 ELRCQCIRTHSTP-FHPKFIKELRVIESPPHCENSEIIVKLTNGNEVCLNPKEKWVQKVV 60
              |||| |: |  ||  ||| : :|:|| : | |   |:|  | || ||||:|:   ::|:|
Db          9 ELRCVCLTT--TPGIHPKTVSDLQVIAAGPQCSKVEVIATLKNGREVCLDPEAPLIKKIV 66

Qy         61 Q 61
              |
Db         67 Q 67


RESULT 14
A28414
melanoma growth-stimulatory activity precursor - human
N;Alternate names: fibroblast-derived neutrophil-activating protein gamma; GRO-alpha; gr
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C;Accession: S13669; A28414; S00983; B60401; S03976; A47626; B46519
R;Baker, N.E.; Kucera, G.; Richmond, A.
Nucleic Acids Res. 18, 6453, 1990
A;Title: Nucleotide sequence of the human melanoma growth stimulatory activity (MGSA) ge
A;Reference number: S13669; MUID:91057157; PMID:2129556
A;Accession: S13669
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-107 <BAK>
A;Cross-references: UNIPROT:P09341; EMBL:X54489; NID:g34625; PIDN:CAA38361.1; PID:g34626
R;Anisowicz, A.; Bardwell, L.; Sager, R.
Proc. Natl. Acad. Sci. U.S.A. 84, 7188-7192, 1987
A;Title: Constitutive overexpression of a growth-regulated gene in transformed Chinese h
A;Reference number: A94184; MUID:88041072; PMID:2890161
A;Accession: A28414
A;Molecule type: mRNA
A;Residues: 1-107 <ANI>
A;Cross-references: GB:J03561; NID:g183622; PIDN:AAA35933.1; PID:g306806
R;Richmond, A.; Balentien, E.; Thomas, H.G.; Flaggs, G.; Barton, D.E.; Spiess, J.; Bordc
EMBO J. 7, 2025-2033, 1988
A;Title: Molecular characterization and chromosomal mapping of melanoma growth stimulatc
A;Reference number: S00983; MUID:88328991; PMID:2970963
A;Accession: S00983
A;Molecule type: mRNA
A;Residues: 1-107 <RIC>
A;Cross-references: EMBL:X12510; NID:g34621; PIDN:CAA31027.1; PID:g34622
R;Schroeder, J.M.; Sticherling, M.; Henneicke, H.H.; Preissner, W.C.; Christophers, E.
J. Immunol. 144, 2223-2232, 1990
A;Title: IL-1alpha or tumor necrosis factor-alpha stimulate release of three NAP-1/IL-8-
A;Reference number: A60401; MUID:90187866; PMID:2179408
A;Accession: B60401
A;Molecule type: protein
A;Residues: 35-42,'X',44,'X',46-48 <SCH>
A;Experimental source: dermal fibroblasts
R;Golds, E.E.; Mason, P.; Nyirkos, P.
Biochem. J. 259, 585-588, 1989
A;Title: Inflammatory cytokines induce synthesis and secretion of gro protein and a neut
A;Reference number: S03975; MUID:89246368; PMID:2655583
A;Accession: S03976
A;Molecule type: protein
A;Residues: 35-41,'X',43-49,'X',51-52,'XX',55-57 <GOL>
R;Schroeder, J.M.; Persoon, N.L.M.; Christophers, E.
J. Exp. Med. 171, 1091-1100, 1990
A;Title: Lipopolysaccharide-stimulated human monocytes secrete, apart from neutrophil-a
ntity with melanoma growth stimulatory activity.
A;Reference number: A47626; MUID:90217938; PMID:2182761
A;Accession: A47626
A;Molecule type: protein
A;Residues: 35-63,'X',65 <SC2>
A;Experimental source: LPS-stimulated monocytes
R;Proost, P.; De Wolf-Peeters, C.; Conings, R.; Opdenakker, G.; Billiau, A.; Van Damme,
J. Immunol. 150, 1000-1010, 1993
A;Title: Identification of a novel granulocyte chemotactic protein (GCP-2) from human t
A;Reference number: A46519; MUID:93139489; PMID:8423327
A;Accession: B46519
A;Molecule type: protein
A;Residues: 35-62 <PRO>
A;Experimental source: MG-63 osteosarcoma cells
C;Genetics:
A;Gene: GDB:GRO1
A;Cross-references: GDB:120181; OMIM:155730
A;Map position: 4q21-4q21
C;Superfamily: beta-thromboglobulin
F;1-34/Domain: signal sequence #status predicted <SIG>
F;35-107/Product: melanoma growth-stimulatory activity #status experimental <MAT>

  Query Match             37.2%;  Score 145.5;  DB 2;  Length 107;
  Best Local Similarity   44.3%;  Pred. No. 2.7e-09;
  Matches   27;  Conservative   11;  Mismatches   22;  Indels    1;  Gaps    1;

Qy          1 TELRCQCIRTHSTPFHPKFIKELRVIESPPHCENSEIIVKLTNGNEVCLNPKEKWVQKVV 60
              |||||||:|     ||| |: : |    |||  :|:|  | || : ||||    |:|::
Db         39 TELRCQCLQT-LQGIHPKNIQSVNVKSPGPHCAQTEVIATLKNGRKACLNPASPIVKKII 97

Qy         61 Q 61
              :
Db         98 E 98


RESULT 15
JH0281
macrophage inflammatory protein 2 alpha precursor - human
N;Alternate names: gro-beta; growth regulated protein beta; melanoma growth-stimulatory
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C;Accession: JH0281; A35931; A38290; A60407
R;Tekamp-Olson, P.; Gallegos, C.; Bauer, D.; McClain, J.; Sherry, B.; Fabre, M.; van Dev
J. Exp. Med. 172, 911-919, 1990
A;Title: Cloning and characterization of cDNAs for murine macrophage inflammatory protei
A;Reference number: JH0200; MUID:90354792; PMID:2201751
A;Accession: JH0281
A;Molecule type: mRNA
A;Residues: 1-107 <TEK>
A;Cross-references: UNIPROT:P19875; GB:X53799; NID:g34658; PIDN:CAA37808.1; PID:g34659
R;Iida, N.; Grotendorst, G.R.
Mol. Cell. Biol. 10, 5596-5599, 1990
A;Title: Cloning and sequencing of a new gro transcript from activated human monocytes:
A;Reference number: A35931; MUID:90377259; PMID:2078213
A;Accession: A35931
A;Molecule type: mRNA
A;Residues: 1-107 <IID>
A;Cross-references: GB:M57731; GB:M36964; NID:g183626; PIDN:AAA63182.1; PID:g183627
R;Haskill, S.; Peace, A.; Morris, J.; Sporn, S.A.; Anisowicz, A.; Lee, S.W.; Smith, T.;
Proc. Natl. Acad. Sci. U.S.A. 87, 7732-7736, 1990
A;Title: Identification of three related human GRO genes encoding cytokine functions.
A;Reference number: A38290; MUID:91017578; PMID:2217207
A;Accession: A38290
A;Molecule type: mRNA
A;Residues: 1-107 <HAS>
A;Cross-references: GB:M36820; NID:g183628; PIDN:AAA63183.1; PID:g183629
R;Sporn, S.A.; Eierman, D.F.; Johnson, C.E.; Morris, J.; Martin, G.; Ladner, M.; Haskill
J. Immunol. 144, 4434-4441, 1990
A;Title: Monocyte adherence results in selective induction of novel genes sharing homolc
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A;Reference number: A60407; MUID:90257367; PMID:2341726
A;Accession: A60407
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 56-107 <SPO>
C;Superfamily: beta-thromboglobulin
C;Keywords: inflammation
F;1-34/Domain: signal sequence #status predicted <SIG>
F;35-107/Product: macrophage inflammatory protein 2 alpha #status predicted <MAT>

Query Match 37.0%; Score 144.5; DB 2; Length 107;
Best Local Similarity 39.7%; Pred. No. 3.5e-09;
Matches 27; Conservative 14; Mismatches 26; Indels 1; Gaps 1;

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Qy          1 TELRCQCIRTHSTPFHPKFIKELRVIESPPHCENSEIIVKLTNGNEVCLNPKEKWVQKVV 60
              |||||||::|     | | |: ::|    |||  :|:|  | || : ||||    |:|::
Db         39 TELRCQCLQT-LQGIHLKNIQSVKVKSPGPHCAQTEVIATLKNGQKACLNPASPMVKKII 97

Qy         61 QVFVKRAE 68
              :  :|  :
Db         98 EKMLKNGK 105
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Search completed: December 13, 2004, 19:53:18
Job time : 38 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: December 13, 2004, 19:35:47 ; Search time 194 Seconds
(without alignments)
213.541 Million cell updates/sec

Title: US-10-087-273-1
Perfect score: 391
Sequence: 1 TELRCQCIRTHSTPFHPKFI.....EKWVQKVVQVFVKRAEKQDP 72

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	379	96.9	101	1	IL8_BOVIN	P79255 bos taurus
2	361	92.3	101	1	IL8_SHEEP	P36925 ovis aries
3	350	89.5	101	1	IL8_CANFA	P41324 canis famil
4	345	88.2	101	2	Q7YRB5	Q7yrb5 tursiops tr
5	335	85.7	103	1	IL8_PIG	P26894 sus scrofa
6	335	85.7	103	2	BAC06611	Bac06611 sus scrof
7	330	84.4	101	1	IL8_RABIT	P19874 oryctolagus
8	312	79.8	101	1	IL8_FELCA	Q9xsx5 felis silve
9	299	76.5	101	1	IL8_MACMU	P51495 macaca mula
10	296	75.7	101	2	Q866R3	Q866r3 equus cabal
11	288	73.7	56	2	Q71UR4	Q71ur4 bos taurus
12	288	73.7	56	2	AAD02808	Aad02808 bos tauru
13	287	73.4	97	2	Q6LAE6	Q6lae6 homo sapien
14	287	73.4	97	2	CAA77745	Caa77745 homo sapi
15	287	73.4	99	1	IL8_HUMAN	P10145 h interleuk
16	287	73.4	99	2	AAP35730	Aap35730 homo sapi
17	285	72.9	97	1	IL8_HORSE	O62812 equus cabal
18	284	72.6	101	1	IL8_CERTO	P46653 cercocebus
19	280	71.6	101	1	IL8_CAVPO	P49113 cavia porce
20	258	66.0	61	2	Q6LAA1	Q6laa1 canis famil
21	258	66.0	61	2	CAA93910	Caa93910 canis fam
22	196	50.1	101	2	Q8UW91	Q8uw91 triakis scy
23	193	49.4	103	1	EMF1_CHICK	P08317 gallus gall
24	193	49.4	103	2	CAB37669	Cab37669 gallus ga
25	192	49.1	104	2	O73912	O73912 gallus gall
26	170	43.5	100	2	Q8AXP4	Q8axp4 chimaera ph
27	165.5	42.3	117	1	AMC2_PIG	P22952 sus scrofa
28	161.5	41.3	96	1	GRO_MOUSE	P12850 mus musculu
29	161.5	41.3	101	1	GRO_CRIGR	P09340 cricetulus
30	155.5	39.8	100	2	Q91ZK9	Q91zk9 sigmodon hi
31	154.5	39.5	96	1	GRO_RAT	P14095 rattus norv
32	154.5	39.5	107	2	Q6PUD4	Q6pud4 sus scrofa
33	154.5	39.5	107	2	AAS91557	Aas91557 sus scrof
34	153.5	39.3	107	2	Q6PUJ1	Q6puj1 sus scrofa
35	153.5	39.3	107	2	AAS90943	Aas90943 sus scrof
36	153	39.1	76	1	AMC_RABIT	P82535 oryctolagus
37	152.5	39.0	101	2	Q91Z64	Q91z64 sigmodon hi
38	149.5	38.2	107	2	Q8HXZ4	Q8hxz4 macaca mula
39	148.5	38.0	107	2	Q8HXZ3	Q8hxz3 macaca mula
40	148.5	38.0	112	1	SZ06_BOVIN	P80221 bos taurus
41	146	37.3	108	2	Q28724	Q28724 oryctolagus
42	145.5	37.2	107	1	GRO_HUMAN	P09341 homo sapien
43	145.5	37.2	107	2	AAP35526	Aap35526 homo sapi
44	144.5	37.0	107	1	MI2A_HUMAN	P19875 homo sapien
45	144.5	37.0	114	1	SZ05_HUMAN	P42830 homo sapien

ALIGNMENTS

```
RESULT 1
IL8_BOVIN
ID   IL8_BOVIN      STANDARD;      PRT;   101 AA.
AC   P79255;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Interleukin-8 precursor (IL-8) (CXCL8).
GN   Name=IL8;
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC   Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96304552; PubMed=8737490;
RA   Morsey M.A., Popowych Y., Kowalski J., Gerlach G., Godson D.,
RA   Campos M., Babiuk L.A.;
RT   "Molecular cloning and expression of bovine interleukin-8.";
RL   Microb. Pathog. 20:203-212(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Galligan C.L., Yoshimura T., Coomber B.L.;
RT   "Cloning and sequencing of bovine interleukin 8 cDNA isolated from
RT   lipopolysaccharide stimulated monocytes in vitro.";
RL   Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: IL-8 is a chemotactic factor that attracts neutrophils,
CC       basophils, and T-cells, but not monocytes. It is also involved in
CC       neutrophil activation. It is released from several cell types in
CC       response to an inflammatory stimulus (By similarity).
CC   -!- SUBUNIT: Homodimer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the intercrine alpha (chemokine CxC)
CC       family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; S82598; AAB37483.1; -.
DR   EMBL; AF232704; AAF37575.1; -.
DR   HSSP; P10145; 1IKM.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0005153; F:interleukin-8 receptor binding; IEP.
DR   GO; GO:0050930; P:induction of positive chemotaxis; IMP.
DR   GO; GO:0042119; P:neutrophil activation; TAS.
DR   GO; GO:0030593; P:neutrophil chemotaxis; IMP.
DR   InterPro; IPR002473; C-X-C/Interlkn_8.
DR   InterPro; IPR001811; Chemokine_IL8.
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DR   InterPro; IPR001089; CXC_chmkine_smll.
DR   Pfam; PF00048; IL8; 1.
DR   PRINTS; PR00436; INTERLEUKIN8.
DR   PRINTS; PR00437; SMALLCYTKCXC.
DR   SMART; SM00199; SCY; 1.
DR   PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.
KW   Chemotaxis; Cytokine; Inflammatory response; Signal.
FT   SIGNAL       1     22       By similarity.
FT   CHAIN       23    101       Interleukin-8.
FT   DISULFID    34     61       By similarity.
FT   DISULFID    36     77       By similarity.
SQ   SEQUENCE   101 AA;  11291 MW;  061A530507906736 CRC64;

  Query Match             96.9%;  Score 379;  DB 1;  Length 101;
  Best Local Similarity   97.2%;  Pred. No. 2.3e-35;
  Matches   70;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TELRCQCIRTHSTPFHPKFIKELRVIESPPHCENSEIIVKLTNGNEVCLNPKEKWVQKVV 60
              ||||||||:|||||||||||||||||||| |||||||||||||||||||||||||||||
Db         30 TELRCQCIKTHSTPFHPKFIKELRVIESGPHCENSEIIVKLTNGNEVCLNPKEKWVQKVV 89

Qy         61 QVFVKRAEKQDP 72
              ||||||||||||
Db         90 QVFVKRAEKQDP 101


RESULT 2
IL8_SHEEP
ID   IL8_SHEEP      STANDARD;      PRT;   101 AA.
AC   P36925;
DT   01-JUN-1994 (Rel. 29, Created)
DT   01-JUN-1994 (Rel. 29, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Interleukin-8 precursor (IL-8) (CXCL8).
GN   Name=IL8;
OS   Ovis aries (Sheep).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC   Caprinae; Ovis.
OX   NCBI_TaxID=9940;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95121931; PubMed=7821808;
RA   Legastelois I., Greenland T., Arnaud P., Mornex J.F., Cordier G.;
RT   "Sequencing of the ovine interleukin-8-encoding cDNA using the
RT   polymerase chain reaction.";
RL   Gene 150:367-369(1994).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95137691; PubMed=7835984;
RA   Seow H.F., Yoshimura T., Wood P.R., Colditz I.G.;
RT   "Cloning, sequencing, expression and inflammatory activity in skin of
RT   ovine interleukin-8.";
RL   Immunol. Cell Biol. 72:398-405(1994).
CC   -!- FUNCTION: IL-8 is a chemotactic factor that attracts neutrophils,
CC       basophils, and T-cells, but not monocytes. It is also involved in
CC       neutrophil activation. It is released from several cell types in
CC       response to an inflammatory stimulus.
CC   -!- SUBUNIT: Homodimer.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the intercrine alpha (chemokine CxC)
CC       family.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X78306; CAA55115.1; -.
DR   EMBL; S74436; AAB33241.1; -.
DR   PIR; S42496; S42496.
DR   HSSP; P10145; 1IKM.
DR   InterPro; IPR002473; C-X-C/Interlkn_8.
DR   InterPro; IPR001811; Chemokine_IL8.
DR   InterPro; IPR001089; CXC_chmkine_smll.
DR   Pfam; PF00048; IL8; 1.
DR   PRINTS; PR00436; INTERLEUKIN8.
DR   PRINTS; PR00437; SMALLCYTKCXC.
DR   SMART; SM00199; SCY; 1.
DR   PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.
KW   Chemotaxis; Cytokine; Inflammatory response; Signal.
FT   SIGNAL       1     22       By similarity.
FT   CHAIN       23    101       Interleukin-8.
FT   DISULFID    34     61       By similarity.
FT   DISULFID    36     77       By similarity.
SQ   SEQUENCE   101 AA;  11292 MW;  40E8418B57C56A5B CRC64;

  Query Match             92.3%;  Score 361;  DB 1;  Length 101;
  Best Local Similarity   91.7%;  Pred. No. 2.6e-33;
  Matches   66;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 TELRCQCIRTHSTPFHPKFIKELRVIESPPHCENSEIIVKLTNGNEVCLNPKEKWVQKVV 60
              ||||||||:|||||||||||||||||||| |||||||||||||||||||||||||||||
Db         30 TELRCQCIKTHSTPFHPKFIKELRVIESGPHCENSEIIVKLTNGKEVCLDPKEKWVQKVV 89

Qy         61 QVFVKRAEKQDP 72
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Db         90 QAFLKRAEKQDP 101


RESULT 3
IL8_CANFA
ID   IL8_CANFA      STANDARD;      PRT;   101 AA.
AC   P41324;
DT   01-FEB-1995 (Rel. 31, Created)
DT   01-FEB-1995 (Rel. 31, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Interleukin-8 precursor (IL-8) (CXCL8).
GN   Name=IL8;
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=94010328; PubMed=7916715;
RA   Ishikawa J., Suzuki S., Hotta K., Hirota Y., Mizuno S., Suzuki K.;
RT   "Cloning of a canine gene homologous to the human interleukin-8-
RT   encoding gene.";
RL   Gene 131:305-306(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lymph node;
RX   MEDLINE=95127913; PubMed=7827282;
RA   Matsumoto Y., Mohamed A., Onodera T., Kato H., Ohashi T., Goitsuka R.,
RA   Tsujimoto H., Hasegawa A., Furusawa S., Yoshihara K., Ishikawa J.,
RA   Hotta K., Suzuki K., Hirota Y.;
RT   "Molecular cloning and expression of canine interleukin 8 cDNA.";
RL   Cytokine 6:455-461(1994).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Mongrel; TISSUE=Jugular vein;
RX   MEDLINE=95114148; PubMed=7814650;
RA   Kukielka G.L., Smith W.C., Larosa G.J., Manning A.M., Mendoza L.H.,
RA   Daly T.J., Hughes B.J., Youker K.A., Hawkins H.K., Michael L.H.,
RA   Rot A., Entman M.L.;
RT   "Interleukin-8 gene induction in the myocardium after ischemia and
RT   reperfusion in vivo.";
RL   J. Clin. Invest. 95:89-103(1995).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Beagle;
RX   MEDLINE=97230298; PubMed=9119462;
```

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RA   Straubinger R.K., Straubinger A.F., Harter L., Jacobson R.H.,
RA   Chang Y.-F., Summers B.A., Erb H.N., Appel M.J.;
RT   "Borrelia burgdorferi migrates into joint capsules and causes an up-
RT   regulation of interleukin-8 in synovial membranes of dogs
RT   experimentally infected with ticks.";
RL   Infect. Immun. 65:1273-1285(1997).
CC   -!- FUNCTION: IL-8 is a chemotactic factor that attracts neutrophils,
CC       basophils, and T-cells, but not monocytes. It is also involved in
CC       neutrophil activation. It is released from several cell types in
CC       response to an inflammatory stimulus.
CC   -!- SUBUNIT: Homodimer.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the intercrine alpha (chemokine CxC)
CC       family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; D28772; BAA05961.1; -.
DR   EMBL; D14285; BAA03246.1; -.
DR   EMBL; U10308; AAC48434.1; -.
DR   EMBL; AF048717; AAC05134.1; -.
DR   HSSP; P10145; 1IKM.
DR   InterPro; IPR002473; C-X-C/Interlkn_8.
DR   InterPro; IPR001811; Chemokine_IL8.
DR   InterPro; IPR001089; CXC_chmkine_sml1.
DR   Pfam; PF00048; IL8; 1.
DR   PRINTS; PR00436; INTERLEUKIN8.
DR   PRINTS; PR00437; SMALLCYTKCXC.
DR   SMART; SM00199; SCY; 1.
DR   PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.
KW   Chemotaxis; Cytokine; Inflammatory response; Signal.
FT   SIGNAL       1     22       By similarity.
FT   CHAIN       23    101       Interleukin-8.
FT   DISULFID    34     61       By similarity.
FT   DISULFID    36     77       By similarity.
SQ   SEQUENCE   101 AA;  11280 MW;  3A3A4676DA968376 CRC64;

  Query Match             89.5%;  Score 350;  DB 1;  Length 101;
  Best Local Similarity   86.1%;  Pred. No. 4.6e-32;
  Matches   62;  Conservative    8;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TELRCQCIRTHSTPFHPKFIKELRVIESPPHCENSEIIVKLTNGNEVCLNPKEKWVQKVV 60
              :|||||||:|||||||||:|||||||:| |||||||||||| |||||||:||||||||||
Db         30 SELRCQCIKTHSTPFHPKYIKELRVIDSGPHCENSEIIVKLFNGNEVCLDPKEKWVQKVV 89

Qy         61 QVFVKRAEKQDP 72
              |:|:|:||||||
Db         90 QIFLKKAEKQDP 101


RESULT 4
Q7YRB5
ID   Q7YRB5      PRELIMINARY;      PRT;   101 AA.
AC   Q7YRB5;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Interlukin-8.
GN   Name=IL-8;
OS   Tursiops truncatus (Atlantic bottle-nosed dolphin).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Delphinidae;
OC   Tursiops.
OX   NCBI_TaxID=9739;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Yosida Y., Shoji Y., Endo T., Ito T., Sakai T.;
RL   Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Yoshida Y., Shoji Y., Endo T., Itou T., Sakai T.;
RL   Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB096002; BAC81421.1; -.
DR   GO; GO:0005576; C:extracellular; IEA.
DR   GO; GO:0008009; F:chemokine activity; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR001811; Chemokine_IL8.
DR   InterPro; IPR001089; CXC_chmkine_sml1.
DR   Pfam; PF00048; IL8; 1.
DR   SMART; SM00199; SCY; 1.
DR   PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.
SQ   SEQUENCE   101 AA;  11370 MW;  2A5DFE251D980E15 CRC64;

  Query Match             88.2%;  Score 345;  DB 2;  Length 101;
  Best Local Similarity   86.1%;  Pred. No. 1.7e-31;
  Matches   62;  Conservative    5;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 TELRCQCIRTHSTPFHPKFIKELRVIESPPHCENSEIIVKLTNGNEVCLNPKEKWVQKVV 60
              :|||||||:|||||||||:|||||||:| |||||||||||| |||||||:||||||||||
Db         30 SELRCQCINIHSTPFHPKFIRELRVIESGPHCENSEIIVKLVNGKEVCLNPKEKWVQKVV 89

Qy         61 QVFVKRAEKQDP 72
              |:|:|:||||||
Db         90 QIFLKRAEKKDP 101


RESULT 5
IL8_PIG
ID   IL8_PIG        STANDARD;      PRT;   103 AA.
AC   P26894; P22951;
DT   01-AUG-1991 (Rel. 19, Created)
DT   01-AUG-1992 (Rel. 23, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Interleukin-8 precursor (IL-8) (CXCL8) (Alveolar macrophage
DE   chemotactic factor I) (AMCF-I).
GN   Name=IL8;
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=94103307; PubMed=8276881;
RA   Lin G., Pearson A.E., Scamurra R.W., Zhou Y., Baarsch M.J.,
RA   Weiss D.J., Murtaugh M.P.;
RT   "Regulation of interleukin-8 expression in porcine alveolar
RT   macrophages by bacterial lipopolysaccharide.";
RL   J. Biol. Chem. 269:77-85(1994).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Sanjanwala M.;
RL   Submitted (JUL-1991) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A., AND SEQUENCE OF 26-45.
RC   TISSUE=Lung;
RX   MEDLINE=93041741; PubMed=1420165;
RA   Goodman R.B., Foster D.C., Mathewes S.L., Osborn S.G., Kuijper J.L.,
RA   Forstrom J.W., Martin T.R.;
RT   "Molecular cloning of porcine alveolar macrophage-derived neutrophil
RT   chemotactic factors I and II; identification of porcine IL-8 and
RT   another intercrine-alpha protein.";
RL   Biochemistry 31:10483-10490(1992).
RN   [4]
RP   REVISION TO 23.
RA   Goodman R.B.;
RL   Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE OF 26-45.
RC   STRAIN=Yorkshire;
RX   MEDLINE=91217086; PubMed=1850745;
```

```
RA   Goodman R.B., Forstrom J.W., Osborn S.G., Chi E.Y., Martin T.R.;
RT   "Identification of two neutrophil chemotactic peptides produced by
RT   porcine alveolar macrophages.";
RL   J. Biol. Chem. 266:8455-8463(1991).
CC   -!- FUNCTION: IL-8 is a chemotactic factor that attracts neutrophils,
CC       basophils, and T-cells, but not monocytes. It is also involved in
CC       neutrophil activation. It is released from several cell types in
CC       response to an inflammatory stimulus.
CC   -!- SUBUNIT: Homodimer.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Alveolar macrophages.
CC   -!- INDUCTION: By lipopolysaccharide (LPS).
CC   -!- SIMILARITY: Belongs to the intercrine alpha (chemokine CxC)
CC       family.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M86923; AAA16616.1; -.
DR   EMBL; X61151; CAA43461.1; -.
DR   EMBL; M99367; AAA92576.1; -.
DR   PIR; A39819; A39819.
DR   PIR; A53096; A53096.
DR   HSSP; P10145; 1IKM.
DR   InterPro; IPR002473; C-X-C/Interlkn_8.
DR   InterPro; IPR001811; Chemokine_IL8.
DR   InterPro; IPR001089; CXC_chmkine_sml1.
DR   Pfam; PF00048; IL8; 1.
DR   PRINTS; PR00436; INTERLEUKIN8.
DR   PRINTS; PR00437; SMALLCYTKCXC.
DR   SMART; SM00199; SCY; 1.
DR   PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.
KW   Chemotaxis; Cytokine; Direct protein sequencing;
KW   Inflammatory response; Signal.
FT   SIGNAL        1     25
FT   CHAIN        26    103       Interleukin-8.
FT   DISULFID     34     61       By similarity.
FT   DISULFID     36     77       By similarity.
FT   CONFLICT     33     34       RC -> CR (in Ref. 5).
FT   CONFLICT     87     87       K -> KK (in Ref. 2).
SQ   SEQUENCE   103 AA;  11633 MW;  9FE0E350E1928C64 CRC64;

  Query Match             85.7%;  Score 335;  DB 1;  Length 103;
  Best Local Similarity   88.4%;  Pred. No. 2.4e-30;
  Matches   61;  Conservative    3;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          2 ELRCQCIRTHSTPFHPKFIKELRVIESPPHCENSEIIVKLTNGNEVCLNPKEKWVQKVVQ 61
              ||||||| |||||||||||||||||| |||||||||||| || ||||:|||||||||||
Db         31 ELRCQCINTHSTPFHPKFIKELRVIESGPHCENSEIIVKLVNGKEVCLDPKEKWVQKVVQ 90

Qy         62 VFVKRAEKQ 70
              :|:|| |||
Db         91 IFLKRTEKQ 99


RESULT 6
BAC06611
ID   BAC06611    PRELIMINARY;      PRT;   103 AA.
AC   BAC06611;
DT   02-MAR-2004 (TrEMBLrel. 27, Created)
DT   02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT   02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE   Interleukin-8.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Shimanuki S., Kobayashi E., Awata T.;
RT   "Genomic structure of the porcine Interleukin 8 gene and development
RT   of a microsatellite marker within intron 1.";
RL   Anim. Genet. 33:470-471(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93041741; PubMed=1420165;
RA   Goodman R., Foster D., Mathewes S., Osborn S., Kuijper J.,
RA   Forstrom J., Martin T.;
RT   "Molecular Cloning of Porcine Alveolar Macrophage-Derived Neutrophil
RT   Chemotactic Factors I and II: Identification of Porcine IL8 and
RT   Another Intercrine-a Protein.";
RL   Biochemistry 31:10483-10490(1992).
DR   EMBL; AB057440; BAC06611.1; -.
SQ   SEQUENCE   103 AA;  11633 MW;  9FE0E350E1928C64 CRC64;

  Query Match             85.7%;  Score 335;  DB 2;  Length 103;
  Best Local Similarity   88.4%;  Pred. No. 2.4e-30;
  Matches   61;  Conservative    3;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          2 ELRCQCIRTHSTPFHPKFIKELRVIESPPHCENSEIIVKLTNGNEVCLNPKEKWVQKVVQ 61
              ||||||| |||||||||||||||||| |||||||||||| || ||||:|||||||||||
Db         31 ELRCQCINTHSTPFHPKFIKELRVIESGPHCENSEIIVKLVNGKEVCLDPKEKWVQKVVQ 90

Qy         62 VFVKRAEKQ 70
              :|:|| |||
Db         91 IFLKRTEKQ 99


RESULT 7
IL8_RABIT
ID   IL8_RABIT      STANDARD;      PRT;   101 AA.
AC   P19874;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-DEC-1992 (Rel. 24, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Interleukin-8 precursor (IL-8) (CXCL8) (Neutrophil
DE   attractant/activation protein-1) (NAP-1) (Permeability factor 1)
DE   (RPF1).
GN   Name=IL8;
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=New Zealand white; TISSUE=Spleen;
RX   MEDLINE=91225489; PubMed=2026877;
RA   Yoshimura T., Yuhki N.;
RT   "Neutrophil attractant/activation protein-1 and monocyte
RT   chemoattractant protein-1 in rabbit. cDNA cloning and their expression
RT   in spleen cells.";
RL   J. Immunol. 146:3483-3488(1991).
RN   [2]
RP   SEQUENCE OF 23-53.
RC   STRAIN=New Zealand white; TISSUE=Peritoneal cavity;
RX   MEDLINE=91058518; PubMed=2244880;
RA   Beaubien B.C., Collins P.D., Jose P.J., Totty N.F., Hsuan J.,
RA   Waterfield M.D., Williams T.J.;
RT   "A novel neutrophil chemoattractant generated during an inflammatory
RT   reaction in the rabbit peritoneal cavity in vivo. Purification,
RT   partial amino acid sequence and structural relationship to interleukin
RT   8.";
RL   Biochem. J. 271:797-801(1990).
CC   -!- FUNCTION: IL-8 is a chemotactic factor that attracts neutrophils,
CC       basophils, and T-cells, but not monocytes. It is also involved in
CC       neutrophil activation. It is released from several cell types in
CC       response to an inflammatory stimulus.
CC   -!- SUBUNIT: Homodimer.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the intercrine alpha (chemokine CxC)
CC       family.
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CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; M57439; AAA31422.1; -.
DR   PIR; I46871; I46871.
DR   HSSP; P10145; 2IL8.
DR   InterPro; IPR002473; C-X-C/Interlkn_8.
DR   InterPro; IPR001811; Chemokine_IL8.
DR   InterPro; IPR001089; CXC_chmkine_sml1.
DR   Pfam; PF00048; IL8; 1.
DR   PRINTS; PR00436; INTERLEUKIN8.
DR   PRINTS; PR00437; SMALLCYTKCXC.
DR   SMART; SM00199; SCY; 1.
DR   PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.
KW   Chemotaxis; Cytokine; Direct protein sequencing;
KW   Inflammatory response; Signal.
FT   SIGNAL        1     22
FT   CHAIN        23    101       Interleukin-8.
FT   DISULFID     34     61       By similarity.
FT   DISULFID     36     77       By similarity.
FT   CONFLICT     50     50       K -> I (in Ref. 2).
SQ   SEQUENCE   101 AA;  11402 MW;  152B110C43AD8726 CRC64;

  Query Match             84.4%;  Score 330;  DB 1;  Length 101;
  Best Local Similarity   83.1%;  Pred. No. 8.9e-30;
  Matches   59;  Conservative    8;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 TELRCQCIRTHSTPFHPKFIKELRVIESPPHCENSEIIVKLTNGNEVCLNPKEKWVQKVV 60
              ||||||||:|||||||||||||||||||| ||| |||||||| :| |:||:||||||||||
Db         30 TELRCQCIKTHSTPFHPKFIKELRVIESGPHCANSEIIVKLVDGRELCLDPKEKWVQKVV 89

Qy         61 QVFVKRAEKQD 71
              |:|:||||:|:
Db         90 QIFLKRAEQQE 100


RESULT 8
IL8_FELCA
ID   IL8_FELCA      STANDARD;      PRT;   101 AA.
AC   Q9XSX5;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Interleukin-8 precursor (IL-8) (CXCL8).
GN   Name=IL8;
OS   Felis silvestris catus (Cat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX   NCBI_TaxID=9685;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Straubinger A.F., Simpson K.W., Straubinger R.K.;
RT   "Feline interleukin-8 mRNA.";
RL   Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: IL-8 is a chemotactic factor that attracts neutrophils,
CC       basophils, and T-cells, but not monocytes. It is also involved in
CC       neutrophil activation. It is released from several cell types in
CC       response to an inflammatory stimulus (By similarity).
CC   -!- SUBUNIT: Homodimer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the intercrine alpha (chemokine CxC)
CC       family.
CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AF158598; AAD40323.1; -.
DR   HSSP; P10145; 1IKM.
DR   InterPro; IPR002473; C-X-C/Interlkn_8.
DR   InterPro; IPR001811; Chemokine_IL8.
DR   InterPro; IPR001089; CXC_chmkine_sml1.
DR   Pfam; PF00048; IL8; 1.
DR   PRINTS; PR00436; INTERLEUKIN8.
DR   PRINTS; PR00437; SMALLCYTKCXC.
DR   SMART; SM00199; SCY; 1.
DR   PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.
KW   Chemotaxis; Cytokine; Inflammatory response; Signal.
FT   SIGNAL        1     22       By similarity.
FT   CHAIN        23    101       Interleukin-8.
FT   DISULFID     34     61       By similarity.
FT   DISULFID     36     77       By similarity.
SQ   SEQUENCE   101 AA;  11165 MW;  690D97F13EF79170 CRC64;

  Query Match             79.8%;  Score 312;  DB 1;  Length 101;
  Best Local Similarity   77.5%;  Pred. No. 1e-27;
  Matches   55;  Conservative   11;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 TELRCQCIRTHSTPFHPKFIKELRVIESPPHCENSEIIVKLTNGNEVCLNPKEKWVQKVV 60
              :|||||||:||||||:|| |||| ||:| |||||||||||| || ||||:||:|||||||
Db         30 SELRCQCIKTHSTPFNPKLIKELTVIDSGPHCENSEIIVKLVNGKEVCLDPKQKWVQKVV 89

Qy         61 QVFVKRAEKQD 71
              ::|:|:||||:
Db         90 EIFLKKAEKQN 100


RESULT 9
IL8_MACMU
ID   IL8_MACMU      STANDARD;      PRT;   101 AA.
AC   P51495;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Interleukin-8 precursor (IL-8) (CXCL8).
GN   Name=IL8;
OS   Macaca mulatta (Rhesus macaque), and
OS   Macaca nemestrina (Pig-tailed macaque).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9544, 9545;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   SPECIES=M.mulatta, and M.nemestrina; TISSUE=Blood;
RX   MEDLINE=96003435; PubMed=7561102;
RA   Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;
RT   "Comparative sequence analysis of cytokine genes from human and
RT   nonhuman primates.";
RL   J. Immunol. 155:3946-3954(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   SPECIES=M.mulatta; TISSUE=Blood;
RX   MEDLINE=95355132; PubMed=7628861;
RA   Minnerly J.C., Baganoff M.P., Deppeler C.L., Keller B.T., Rapp S.R.,
RA   Widomski D.L., Fretland D.J., Bolanowski M.A.;
RT   "Identification and characterization of rhesus macaque interleukin-
RT   8.";
RL   Inflammation 19:313-331(1995).
CC   -!- FUNCTION: IL-8 is a chemotactic factor that attracts neutrophils,
CC       basophils, and T-cells, but not monocytes. It is also involved in
CC       neutrophil activation. It is released from several cell types in
CC       response to an inflammatory stimulus (By similarity).
CC   -!- SUBUNIT: Homodimer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the intercrine alpha (chemokine CxC)
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CC       family.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U19849; AAA86711.1; -.
DR   EMBL; U19851; AAA86713.1; -.
DR   EMBL; S78555; AAA80141.2; -.
DR   HSSP; P10145; 2IL8.
DR   InterPro; IPR002473; C-X-C/Interlkn_8.
DR   InterPro; IPR001811; Chemokine_IL8.
DR   InterPro; IPR001089; CXC_chmkine_sml1.
DR   Pfam; PF00048; IL8; 1.
DR   PRINTS; PR00436; INTERLEUKIN8.
DR   PRINTS; PR00437; SMALLCYTKCXC.
DR   SMART; SM00199; SCY; 1.
DR   PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.
KW   Chemotaxis; Cytokine; Inflammatory response; Signal.
FT   SIGNAL        1     22       By similarity.
FT   CHAIN        23    101       Interleukin-8.
FT   DISULFID     34     61       By similarity.
FT   DISULFID     36     77       By similarity.
SQ   SEQUENCE   101 AA;  11320 MW;  42BCF9C97C84B5F9 CRC64;

  Query Match             76.5%;  Score 299;  DB 1;  Length 101;
  Best Local Similarity   74.6%;  Pred. No. 3.1e-26;
  Matches   53;  Conservative   11;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          2 ELRCQCIRTHSTPFHPKFIKELRVIESPPHCENSEIIVKLTNGNEVCLNPKEKWVQKVVQ 61
              ||||:||:|:| |||||||||||||| ||| |:||||||::| |:||:||| |||:||:
Db         31 ELRCECIKTYSKPFHPKFIKELRVIESGPHCANTEIIVKLSDGRELCLDPKEPWVQRVVE 90

Qy         62 VFVKRAEKQDP 72
              |||||| |:|
Db         91 KFVKRAENQNP 101


RESULT 10
Q866R3
ID   Q866R3      PRELIMINARY;      PRT;   101 AA.
AC   Q866R3;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Interleukin 8.
GN   Name=IL8;
OS   Equus caballus (Horse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX   NCBI_TaxID=9796;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Cappelli K., Verini-Supplizi A., Silvestrelli M.;
RL   Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY184956; AAO37764.1; -.
DR   HSSP; P10145; 2IL8.
DR   GO; GO:0005576; C:extracellular; IEA.
DR   GO; GO:0008009; F:chemokine activity; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR002473; C-X-C/Interlkn_8.
DR   InterPro; IPR001811; Chemokine_IL8.
DR   InterPro; IPR001089; CXC_chmkine_sml1.
DR   Pfam; PF00048; IL8; 1.
DR   PRINTS; PR00436; INTERLEUKIN8.
DR   PRINTS; PR00437; SMALLCYTKCXC.
DR   SMART; SM00199; SCY; 1.
DR   PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.
SQ   SEQUENCE   101 AA;  11080 MW;  E34878111854009A CRC64;

  Query Match             75.7%;  Score 296;  DB 2;  Length 101;
  Best Local Similarity   76.1%;  Pred. No. 6.8e-26;
  Matches   54;  Conservative    6;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          2 ELRCQCIRTHSTPFHPKFIKELRVIESPPHCENSEIIVKLTNGNEVCLNPKEKWVQKVVQ 61
              |||||||:||| ||:|| |||:| ||| |||||||||||| || ||||||  |||| :||
Db         31 ELRCQCIKTHSKPFNPKLIKEMRAIESGPHCENSEIIVKLVNGAEVCLNPHTKWVQIIVQ 90

Qy         62 VFVKRAEKQDP 72
              |:|||| |:|
Db         91 AFLKRAEGQNP 101


RESULT 11
Q71UR4
ID   Q71UR4      PRELIMINARY;      PRT;    56 AA.
AC   Q71UR4;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Interleukin-8 (Fragment).
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC   Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99122841; PubMed=9922392;
RA   Heaton M.P., Laegreid W.W., Beattie C.W., Smith T.P.L., Kappes S.M.;
RT   "Identification and genetic mapping of bovine chemokine genes
RT   expressed in epithelial cells.";
RL   Mamm. Genome 10:128-133(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21189989; PubMed=11252171;
RA   Heaton M.P., McKown C.G., Grosse W.M., Keen J.E., Fox J.M.,
RA   Laegreid W.W.;
RT   "Interleukin-8 haplotype structure from nucleotide sequence variation
RT   in commercial populations of US cattle.";
RL   Mamm. Genome 12:219-226(2001).
DR   EMBL; AF061521; AAD02808.1; -.
DR   InterPro; IPR002473; C-X-C/Interlkn_8.
DR   InterPro; IPR001811; Chemokine_IL8.
DR   InterPro; IPR001089; CXC_chmkine_sml1.
DR   Pfam; PF00048; IL8; 1.
DR   PRINTS; PR00436; INTERLEUKIN8.
DR   PRINTS; PR00437; SMALLCYTKCXC.
DR   SMART; SM00199; SCY; 1.
FT   NON_TER       1      1
SQ   SEQUENCE   56 AA;  6474 MW;  827ACE2DAAA784E3 CRC64;

  Query Match             73.7%;  Score 288;  DB 2;  Length 56;
  Best Local Similarity   98.2%;  Pred. No. 2.9e-25;
  Matches   55;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         17 PKFIKELRVIESPPHCENSEIIVKLTNGNEVCLNPKEKWVQKVVQVFVKRAEKQDP 72
              ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db          1 PKFIKELRVIESGPHCENSEIIVKLTNGNEVCLNPKEKWVQKVVQVFVKRAEKQDP 56


RESULT 12
AAD02808
ID   AAD02808    PRELIMINARY;      PRT;    56 AA.
AC   AAD02808;
DT   02-MAR-2004 (TrEMBLrel. 27, Created)
DT   02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT   02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE   Interleukin-8 (Fragment).
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99122841; PubMed=9922392;
RA   Heaton M.P., Laegreid W.W., Beattie C.W., Smith T.P.L., Kappes S.M.;
RT   "Identification and genetic mapping of bovine chemokine genes
RT   expressed in epithelial cells.";
RL   Mamm. Genome 10:128-133(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Heaton M.P., McKown C.G., Grosse W.M., Keen J.E., Fox J.M.,
RA   Laegreid W.W.;
RT   "Interleukin-8 haplotype structure from nucleotide sequence variation
RT   in commercial populations of US cattle.";
RL   Mamm. Genome 12:219-225(2001).
DR   EMBL; AF061521; AAD02808.1; -.
FT   NON_TER       1      1
SQ   SEQUENCE   56 AA;  6474 MW;  827ACE2DAAA784E3 CRC64;

  Query Match             73.7%;  Score 288;  DB 2;  Length 56;
  Best Local Similarity   98.2%;  Pred. No. 2.9e-25;
  Matches   55;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         17 PKFIKELRVIESPPHCENSEIIVKLTNGNEVCLNPKEKWVQKVVQVFVKRAEKQDP 72
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db          1 PKFIKELRVIESGPHCENSEIIVKLTNGNEVCLNPKEKWVQKVVQVFVKRAEKQDP 56


RESULT 13
Q6LAE6
ID   Q6LAE6      PRELIMINARY;      PRT;    97 AA.
AC   Q6LAE6;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Interleukin 8 (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RX   MEDLINE=91374977; PubMed=1895676;
RA   Kusner D.J., Luebbers E.L., Nowinski R.J., Konieczkowski M.,
RA   King C.H., Sedor J.R.;
RT   "Cytokine- and LPS-induced synthesis of interleukin-8 from human
RT   mesangial cells.";
RL   Kidney Int. 39:1240-1248(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RA   King C.H., Gordon G.S., Konieczkowski M., Sedor J.R.;
RL   Submitted (FEB-1992) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RA   King C.;
RL   Submitted (FEB-1992) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; Z11686; CAA77745.1; -.
DR   InterPro; IPR002473; C-X-C/Interlkn_8.
DR   InterPro; IPR001811; Chemokine_IL8.
DR   InterPro; IPR001089; CXC_chmkine_sml1.
DR   Pfam; PF00048; IL8; 1.
DR   PRINTS; PR00436; INTERLEUKIN8.
DR   PRINTS; PR00437; SMALLCYTKCXC.
DR   SMART; SM00199; SCY; 1.
DR   PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.
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  Matches   51;  Conservative   10;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          2 ELRCQCIRTHSTPFHPKFIKELRVIESPPHCENSEIIVKLTNGNEVCLNPKEKWVQKVVQ 61
              |||||||:|:| ||||||||||||||| ||| |:||||||::| |:||:||| |||:||:
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Qy         62 VFVKRAE 68
              |:||||
Db         91 KFLKRAE 97


RESULT 14
CAA77745
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AC   CAA77745;
DT   02-MAR-2004 (TrEMBLrel. 27, Created)
DT   02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT   02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE   Interleukin 8 (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney, cortex;
RA   King C.H., Gordon G.S., Konieczkowski M., Sedor J.R.;
RT   "cDNA cloning of human mesangial cell interleukin 8 by polymerase
RT   chain reaction.";
RL   Submitted (FEB-1992) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney, cortex;
RX   MEDLINE=91374977; PubMed=1895676;
RA   Kusner D.J., Luebbers E.L., Nowinski R.J., Konieczkowski M.,
RA   King C.H., Sedor J.R.;
RT   "Cytokine- and LPS-induced synthesis of interleukin-8 from human
RT   mesangial cells.";
RL   Kidney Int. 39:1240-1248(1991).
DR   EMBL; Z11686; CAA77745.1; -.
FT   NON_TER       1      1
FT   NON_TER      97     97
SQ   SEQUENCE   97 AA;  10897 MW;  09996E89319F4972 CRC64;

  Query Match             73.4%;  Score 287;  DB 2;  Length 97;
  Best Local Similarity   76.1%;  Pred. No. 6.9e-25;
  Matches   51;  Conservative   10;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          2 ELRCQCIRTHSTPFHPKFIKELRVIESPPHCENSEIIVKLTNGNEVCLNPKEKWVQKVVQ 61
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Qy         62 VFVKRAE 68
              |:||||
Db         91 KFLKRAE 97


RESULT 15
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ID   IL8_HUMAN      STANDARD;      PRT;    99 AA.
AC   P10145; Q96RG6; Q9C077;
DT   01-MAR-1989 (Rel. 10, Created)
DT   01-MAR-1989 (Rel. 10, Last sequence update)
DT   01-OCT-2004 (Rel. 45, Last annotation update)
DE   Interleukin-8 precursor (IL-8) (CXCL8) (Monocyte-derived neutrophil
DE   chemotactic factor) (MDNCF) (T-cell chemotactic factor) (Neutrophil-
DE   activating protein 1) (NAP-1) (Protein 3-10C) (Granulocyte chemotactic
DE   protein 1) (GCP-1) (Monocyte derived neutrophil activating peptide)
DE   (MONAP) (Emoctakin) [Contains: MDNCF-a (IL8/NAP1 form I) (GCP/IL-8
DE   protein IV); IL-8(1-77) (MDNCF-b) (IL8/NAP1 form II) (GCP/IL-8 protein
DE   II) ((ala-IL-8)77); IL-8(6-77) (Lymphocyte-derived neutrophil-
```

DE activating factor) (LYNAP) (Neutrophil-activating factor) (NAF)
DE (MDNCF-c) (IL8/NAP1 form III) (GCP/IL-8 protein I) ((ser-IL-8)72); IL-
DE 8(7-77) (IL8/NAP1 form IV) (GCP/IL-8 protein V); IL-8(8-77) (IL8/NAP1
DE form V) (GCP/IL-8 protein VI); IL-8(9-77) (IL8/NAP1 form VI) (GCP/IL-8
DE protein III)].
GN Name=IL8;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88258376; PubMed=3260265;
RA Matsushima K., Morishita K., Yoshimura T., Lavu S., Kobayashi Y.,
RA Lew W., Appella E., Kung H., Leonard E.J., Oppenheim J.J.;
RT "Molecular cloning of a human monocyte-derived neutrophil chemotactic
RT factor (MDNCF) and the induction of MDNCF mRNA by interleukin 1 and
RT tumor necrosis factor.";
RL J. Exp. Med. 167:1883-1893(1988).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87224164; PubMed=2953813;
RA Schmid J., Weissmann C.;
RT "Induction of mRNA for a serine protease and a beta-thromboglobulin-
RT like protein in mitogen-stimulated human leukocytes.";
RL J. Immunol. 139:250-256(1987).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=89313739; PubMed=2664463;
RA Kowalski J., Denhardt D.T.;
RT "Regulation of the mRNA for monocyte-derived neutrophil-activating
RT peptide in differentiating HL60 promyelocytes.";
RL Mol. Cell. Biol. 9:1946-1957(1989).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=89309826; PubMed=2663993;
RA Mukaida N., Shiroo M., Matsushima K.;
RT "Genomic structure of the human monocyte-derived neutrophil
RT chemotactic factor IL-8.";
RL J. Immunol. 143:1366-1371(1989).
RN [5]
RP SEQUENCE FROM N.A.
RA Ishikawa J.;
RL Submitted (JAN-1993) to the EMBL/GenBank/DDBJ databases.
RN [6]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RA Jang J.S., Kim B.E.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RA Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,
RA Nickerson D.A.;
RT "SeattleSNPs. NHLBI HL66682 program for genomic applications, UW-
RT FHCRC, Seattle, WA (URL: http://pga.gs.washington.edu).";
RL Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
RN [8]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [9]
RP SEQUENCE OF 21-32, IDENTIFICATION OF MDNCF-A; IL-8(1-77) AND
RP IL-8(6-77), AND N-TERMINAL PROCESSING.
RX PubMed=2648135;
RA Yoshimura T., Robinson E.A., Appella E., Matsushima K.,
RA Showalter S.D., Skeel A., Leonard E.J.;
RT "Three forms of monocyte-derived neutrophil chemotactic factor (MDNCF)
RT distinguished by different lengths of the amino-terminal sequence.";
RL Mol. Immunol. 26:87-93(1989).
RN [10]
RP SEQUENCE OF 23-46, AND IDENTIFICATION OF IL-8(1-77).
RX MEDLINE=89246368; PubMed=2655583;
RA Golds E.E., Mason P., Nyirkos P.;
RT "Inflammatory cytokines induce synthesis and secretion of gro protein
RT and a neutrophil chemotactic factor but not beta 2-microglobulin in
RT human synovial cells and fibroblasts.";
RL Biochem. J. 259:585-588(1989).
RN [11]
RP SEQUENCE OF 23-54, AND IDENTIFICATION OF IL-8(1-77).
RX MEDLINE=89279141; PubMed=2659722;
RA Suzuki K., Miyasaka H., Ota H., Yamakawa Y., Tagawa M., Kuramoto A.,
RA Mizuno S.;
RT "Purification and partial primary sequence of a chemotactic protein
RT for polymorphonuclear leukocytes derived from human lung giant cell
RT carcinoma LU65C cells.";
RL J. Exp. Med. 169:1895-1901(1989).
RN [12]
RP SEQUENCE OF 28-99, AND IDENTIFICATION OF IL-8(6-77).
RX MEDLINE=88162914; PubMed=3279957;
RA Gregory H., Young J., Schroeder J.-M., Mrowietz U., Christophers E.;
RT "Structure determination of a human lymphocyte derived neutrophil
RT activating peptide (LYNAP).";
RL Biochem. Biophys. Res. Commun. 151:883-890(1988).
RN [13]
RP SEQUENCE OF 28-59, AND IDENTIFICATION OF IL-8(6-77).
RX MEDLINE=88106502; PubMed=3322281;
RA Walz A., Peveri P., Aschauer H., Baggiolini M.;
RT "Purification and amino acid sequencing of NAF, a novel neutrophil-
RT activating factor produced by monocytes.";
RL Biochem. Biophys. Res. Commun. 149:755-761(1987).
RN [14]
RP SEQUENCE OF 28-69, AND IDENTIFICATION OF IL-8(6-77).
RX MEDLINE=88097462; PubMed=3480540;
RA Yoshimura T., Matsushima K., Tanaka S., Robinson E.A., Appella E.,
RA Oppenheim J.J., Leonard E.J.;
RT "Purification of a human monocyte-derived neutrophil chemotactic
RT factor that has peptide sequence similarity to other host defense
RT cytokines.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:9233-9237(1987).
RN [15]
RP SEQUENCE OF 21-41, IDENTIFICATION OF MDNCF-A; IL-8(1-77); IL-8(6-77);
RP IL-8(7-77); IL-8(8-77) AND IL-8(9-77), N-TERMINAL PROCESSING, AND
RP FUNCTION.
RX MEDLINE=91006326; PubMed=2145175;
RA van Damme J., Rampart M., Coning R., Decock B., van Osselaer N.,
RA Willems J., Billiau A.;
RT "The neutrophil-activating proteins interleukin 8 and beta-
RT thromboglobulin: in vitro and in vivo comparison of NH2-terminally
RT processed forms.";
RL Eur. J. Immunol. 20:2113-2118(1990).
RN [16]
RP SEQUENCE OF 21-41, IDENTIFICATION OF MDNCF-A; IL-8(1-77); IL-8(6-77);
RP IL-8(7-77); IL-8(8-77) AND IL-8(9-77), AND N-TERMINAL PROCESSING.
RX MEDLINE=89231715; PubMed=2523801;
RA van Damme J., van Beeumen J., Conings R., Decock B., Billiau A.;
RT "Purification of granulocyte chemotactic peptide/interleukin-8 reveals
RT N-terminal sequence heterogeneity similar to that of beta-

RT thromboglobulin.";
RL Eur. J. Biochem. 181:337-344(1989).
RN [17]
RP N-TERMINAL PROCESSING BY THROMBIN, AND FUNCTION.
RX PubMed=2212672;
RA Hebert C.A., Luscinskas F.W., Kiely J.-M., Luis E.A., Darbonne W.C.,
RA Bennett G.L., Liu C.C., Obin M.S., Gimbrone M.A. Jr., Baker J.B.;
RT "Endothelial and leukocyte forms of IL-8. Conversion by thrombin and
RT interactions with neutrophils.";
RL J. Immunol. 145:3033-3040(1990).
RN [18]
RP SYNTHESIS OF 28-99.
RX MEDLINE=91175767; PubMed=2007144;
RA Clark-Lewis I., Mose B., Walz A., Baggiolini M., Scott G.J.,
RA Aebersold R.;
RT "Chemical synthesis, purification, and characterization of two
RT inflammatory proteins, neutrophil activating peptide 1 (interleukin-8)
RT and neutrophil activating peptide.";
RL Biochemistry 30:3128-3135(1991).
RN [19]
RP N-TERMINAL PROCESSING BY MMP9.
RX PubMed=11023497;
RA Van den Steen P.E., Proost P., Wuyts A., Van Damme J., Opdenakker G.;
RT "Neutrophil gelatinase B potentiates interleukin-8 tenfold by
RT aminoterminal processing, whereas it degrades CTAP-III, PF-4, and GRO-
RT alpha and leaves RANTES and MCP-2 intact.";
RL Blood 96:2673-2681(2000).
RN [20]
RP REVIEW.
RX MEDLINE=92347562; PubMed=1639201;
RA Baggiolini M., Clark-Lewis I.;
RT "Interleukin-8, a chemotactic and inflammatory cytokine.";
RL FEBS Lett. 307:97-101(1992).
RN [21]
RP REVIEW.
RX PubMed=14711052;
RA Struyf S., Proost P., Van Damme J.;
RT "Regulation of the immune response by the interaction of chemokines
RT and proteases.";
RL Adv. Immunol. 81:1-44(2003).
RN [22]
RP STRUCTURE BY NMR OF 28-99.

Query Match 73.4%; Score 287; DB 1; Length 99;
Best Local Similarity 76.1%; Pred. No. 7e-25;
Matches 51; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

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